

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:02:32 ; Search time 34.92 seconds
(without alignments)
7.778 Million cell updates/sec

Title: US-09-687-267-6

Perfect score: 12

Sequence: 1 XXXC 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	3	A22565	R-phycoerythrin al
2	9	75.0	4	I51049	metallothionein-A
3	9	75.0	4	S43959	Ig mu chain V regi
4	9	75.0	4	S5238	pallidipin - assas
5	9	75.0	5	A22565	R-phycoerythrin al
6	9	75.0	5	F22565	R-phycoerythrin ga
7	9	75.0	5	A3882	cadmium-binding pe
8	9	75.0	5	B45525	actin I - malaria
9	9	75.0	5	S65726	hemoglobin, extrac
10	9	75.0	6	JU0355	lipopeptide wsl279
11	9	75.0	6	A22565	R-phycoerythrin be
12	9	75.0	6	I37027	protamine P1 - gor
13	9	75.0	6	I37263	Y protein - human
14	9	75.0	6	S29881	Na+/K+-exchanging
15	9	75.0	6	H48394	glycoprotein compo
16	9	75.0	6	I67345	MHC H2-K-k cell su
17	9	75.0	6	I65546	MHC H2-L antigen -
18	9	75.0	6	PT0652	T-cell receptor be
19	9	75.0	6	F1946	T-cell receptor ga
20	9	75.0	6	I49421	laminin B1 - weste
21	9	75.0	6	I79564	hypothetical TGL3
22	9	75.0	7	PH1408	Ig heavy chain V r
23	9	75.0	7	A58512	venom heptapeptide
24	9	75.0	7	S08606	hypothetical prote
25	9	75.0	7	S38516	mablin II chain
26	9	75.0	7	B34818	vicilin 57K chain
27	9	75.0	7	B33882	cadmium-binding he
28	9	75.0	7	A34026	acetylcholinestera
29	9	75.0	7	A12016	formylglycinamide

30 9 75.0 7 2 PH1602 Ig H chain V-D-J r
31 9 75.0 7 2 PH0932 T-cell receptor be
32 7 4 I56695 hypothetical I2 pr
33 9 75.0 8 2 PH1407 Ig heavy chain V r
34 9 75.0 8 2 S59622 metallothionein is
35 9 75.0 8 2 XGHUEU urine glycopeptide
36 9 75.0 8 2 A25836 L-serine dehydrata
37 9 75.0 8 2 PC1002 leucine--trNA liga
38 9 75.0 8 2 S19288 acylase - Kluyvera
39 9 75.0 8 2 A37521 R-phycoerythrin ga
40 9 75.0 8 2 C61512 variant surface gl
41 9 75.0 8 2 D61512 variant surface gl
42 9 75.0 8 2 PH1618 Ig H chain V-D-J r
43 9 75.0 8 2 PH0803 T-cell receptor al
44 9 75.0 8 2 I57018 gene Cfr protein
45 9 75.0 8 2 PH0934 T-cell receptor be

ALIGNMENTS

RESULT 1

A22565

R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: A22565

R.Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: A22565

A:Molecule type: protein

A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

Db 1 C 1

RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51049

R.Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; MUID:95324545

A:Accession: I51049

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

Db 4 C 4

RESULT 3

S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 2 C 2

RESULT 4

S55238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S55238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib
A:Reference number: S55238; MUID:95251610
A:Accession: S55238
A:Molecule type: protein
A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 3 C 3

RESULT 5

B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 2 C 2

RESULT 6

F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: F22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 3 C 3

RESULT 7

A33882
cadmium-binding pentapeptide - downy thornapple
C:Species: Datura innoxia (downy thornapple)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C:Accession: A33882
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in pla
A:Reference number: A94182; MUID:88016144
A:Accession: A33882
A:Molecule type: protein
A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 2 C 2

RESULT 8

B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: B45525
R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen
Mol. Biochem. Parasitol. 35, 167-176, 1989
A:Title: Stage-specific expression and genomic organization of the actin genes of the
A:Reference number: A45525; MUID:89364996
A:Accession: B45525
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <WES>
A:Cross-references: GB:J03988
A:Note: the authors translated the codon GAA for residue 3 as Gly
C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 4 C 4

RESULT 9

S65726
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65726
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A:Reference number: S65721; MUID:96176855
A:Accession: S65726
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 4 C 4

RESULT 10

JU0355
lipopeptide WS1279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JU0355
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin
A:Reference number: JU0355; MUID:91300586
A:Accession: JU0355
A:Molecule type: protein
A:Residues: 1-6 <TSU>
A>Note: the structure was confirmed by synthesis
C:Keywords: blocked amino end; lipoprotein
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 1 C 1

RESULT 11

C22565
R-phycoerythrin beta-1 chain - red alga (Gastrocionium coulteri) (fragment)
C:Species: Gastrocionium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 4 C 4

RESULT 12

137027
protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: I37013; MUID:94040810
A:Accession: I37027
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 6 C 6

RESULT 13

I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternate
A:Reference number: I37263; MUID:93010891
A:Accession: I37263
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4

Db 4 C 4

RESULT 14

S29881
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S29881
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases from
A:Reference number: S29881; MUID:85131201
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney

C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 2 C 2

RESULT 15

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fa
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Author, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 6 C 6

Search completed: February 5, 2001, 12:02:33
Job time: 290 sec

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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:06:02 ; Search time 20.72 Seconds
(without alignments)
6.234 Million cell updates/sec

Title: US-09-687-267-6
Perfect score: 12
Sequence: 1 XXXX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	9	75.0	8 1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8 1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9 1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9 1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9 1 CONO_CONST	P05487 conus stria
6	9	75.0	9 1 DNFL_LOCM1	P16339 locusta mig
7	9	75.0	9 1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9 1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9 1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9 1 OXYA_SQUAC	P42997 squalus aca
11	9	75.0	9 1 OXYF_SCYCA	P42997 scyllorhinu
12	9	75.0	9 1 OXYT_BUFRE	P42995 bufo regula
13	9	75.0	9 1 OXYT_CYPCA	P23879 cyprinus ca
14	9	75.0	9 1 OXYT_EISFO	P42998 eisenia foe
15	9	75.0	9 1 OXYT_OCTUV	P80027 octopus vul
16	9	75.0	9 1 OXYT_RABIT	P32878 oryctolagus
17	9	75.0	9 1 OXYT_RAJCL	P42994 raja clavav
18	9	75.0	9 1 OXYV_SQUAC	P43000 squalus aca
19	9	75.0	9 1 RSLI_SALTY	O54296 salmonella
20	9	75.0	9 1 SAP_STOVA	P24047 stomopneute
21	9	75.0	9 1 TAL1_PICJA	P17440 pichia jadi
22	9	75.0	9 1 TAL3_PICJA	P17441 pichia jadi
23	9	75.0	10 1 GLEM_HUMAN	P02728 homo sapien
24	9	75.0	10 1 GON2_CHEPR	P80678 cheilosoma
25	9	75.0	10 1 RCA_PINPS	P81084 pinus pinas
26	9	75.0	12 1 CXAL_CONTM	P50983 conus imper
27	9	75.0	12 1 N040_LOTJA	O22426 lotus japon
28	9	75.0	12 1 N040_SESRO	O24369 sesbania ro
29	9	75.0	12 1 N040_SOYBN	P55960 glycine max
30	9	75.0	12 1 RRI6_GINBI	P36207 ginkgo bilo
31	9	75.0	12 1 TAL0_TREME	P01371 tremella me
32	9	75.0	12 1 UR2A_CATCO	P04558 catostomus
33	9	75.0	12 1 UR2B_CATCO	P04559 catostomus

34	9	75.0	12 1 UR2B_CYPCA	P04561 cyprinus ca
35	9	75.0	12 1 UR2_GILMI	P01147 gillichthys
36	9	75.0	12 1 UR2_POLSP	P81022 polyodon sp
37	9	75.0	12 1 UR2_SCYCA	P35490 scyllorhinu
38	9	75.0	12 1 YZPY_ECOLI	P17776 escherichia
39	9	75.0	13 1 ACT7_SOYBN	P15987 glycine max
40	9	75.0	13 1 CXAL_CONST	P15471 conus stria
41	9	75.0	13 1 CXAA2_CONGE	P01520 conus geogr
42	9	75.0	13 1 CXAA2_CONST	P28878 conus stria
43	9	75.0	13 1 CXET_CONTE	P81755 conus texti
44	9	75.0	13 1 GER1_HORVU	P28525 hordeum vul
45	9	75.0	13 1 GER2_HORVU	P28526 hordeum vul

ALIGNMENTS

RESULT 1

ID	ACT_CARMA	STANDARD;	PRT;	8 AA.
AC	P80709;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ACTIN (FRAGMENT).			
OS	Carcinus maenas (Common shore crab) (Green crab).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eubrachyura; Portunoidae; Fortunidae; Carcinus.			
RN	[1]			
RP	SEQUENCE.			
RA	Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,			
RA	Baghdassarian D.;			
RT	"A. transaldolase. An enzyme implicated in crab steroidogenesis."			
RL	Endocrine 5:23-32(1996).			
CC	-!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED			
CC	IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED			
CC	IN ALL EUKARYOTIC CELLS.			
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:			
CC	6.8, ITS MW IS: 46 KDA.			
CC	-!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.			
CC	INTERPRO: IPR000279; .			
DR	PROSITE: PS00405; ACTINS_1; PARTIAL.			
DR	PROSITE: PS00432; ACTINS_2; PARTIAL.			
DR	PROSITE: PS01132; ACTINS_ACT-LIKE; PARTIAL.			
KW	Structural protein.			
FT	NON_TER 1 1			
FT	NON_TER 8 8			
SQ	SEQUENCE 8 AA: 976 MW: 1424005AB2CAAE3 CRC64;			

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4 C 4
Db	2 C 2

RESULT 2

ID	GLUR_HUMAN	STANDARD;	PRT;	8 AA.
ID	P02729;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	URINE GLYCOPETIDE.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			

```
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
   glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25P-25P(1971).
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
   IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
   ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
   SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
CC KW Glycoprotein.
DR PIR; A03188; XGHUEU.
FT CARBOHYD
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 3
CONO_CONGE STANDARD; PRT; 9 AA.
ID CCAP_CARMA
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CARDIOACTIVE PEPTIDE (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RX SPECIES=C.MAENAS; TISSUE=PERICARDIAL ORGANS;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
   shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RX SPECIES=M.SEXTA;
RA MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
   hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RX SPECIES=T.MOLITOR, AND S.ERIDANIA; TISSUE=HEAD;
RA MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
   molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
   INTO THE HEMOLYPH.
DR PIR; A26363; A26363.
DR PIR; A26363; A26363.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 5
CONO_CONGE STANDARD; PRT; 9 AA.
ID CONO_CONGE
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LYS-CONOPRESSIN G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
   peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR INTERPRO; IPR000981;
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT AMIDATION.
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 5
CONO_CONGE STANDARD; PRT; 9 AA.
ID CONO_CONGE
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ARG-CONOPRESSIN S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.;
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
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RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]

RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B28495; B28495.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 6
DNFL_LOCFI STANDARD; PRT; 9 AA.
AC F16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
RN [1]
RP SEQUENCE.
RC TISSUE=SUBOESOPHAGEAL GANGLION, AND THORACIC GANGLION;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RT Locusta migratoria";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -!- FUNCTION: DIURETIC HORMONE.
CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A29477; A29477.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6
FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 7
ISOT_CYPCA STANDARD; PRT; 9 AA.
ID ISOT_CYPCA
AC P42993;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ISOTOCIN.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PIUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes";
RL Comp. Biochem. Physiol. 14:245-254(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A61364; A61364.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 8
MGMT_BOVIN STANDARD; PRT; 9 AA.
ID MGMT_BOVIN
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=THYMUS;
RX MEDLINE=90174912; PubMed=23088822;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
CC IRREVERSIBLY INACTIVATED.
CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN
CC L-CYSTEINE = DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-
CC L-CYSTEINE.
CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR INTERPRO: IPR001497; -.

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DR PROSITE: PS00374; MGMT: PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 3251171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 9 C 9

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE
RC TISSUE=PITUITARY;
RA Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 10
ID OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPATOCIN (ASPATOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
Acher R., Chauvet J., Chauvet M.-T.;
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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=95062247; PubMed=7972045;
Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus caniculus).";
Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 1 C 1

RESULT 12
OXYT_BUFRE
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ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE SERITOCIN.
OS Bufo regularis (African toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufonidae;
OC Bufo.
RN [1]
RP SEQUENCE.
RC TISSUE-PITUITARY NEUROINTERMEDIATE LOBE;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 983 MW; 17FF476E5A5A6D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 1 C 1

RESULT 13
OXYT_CYPCA STANDARD; PRT; 9 AA.
ID OXYT_CYPCA
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1991 (Rel. 32, Last annotation update)
DE VASOTOCIN.
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C.CARPIO; TISSUE-PITUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P.MARINUS; TISSUE-PITUITARY;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): Isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR INTERPRO; IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 1 C 1

RESULT 15
OXYT_OCTVU STANDARD; PRT; 9 AA.
ID OXYT_OCTVU
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CEPHALOTOCIN.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
RN [1]
RP SEQUENCE.
RC TISSUE-NERVE ENDINGS;

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RX MEDLINE=92270139; PubMed=1589145;
 RA Reich G.;
 RT "A new peptide of the oxytocin/vasopressin family isolated from
 RL nerves of the cephalopod Octopus vulgaris.";
 RL Neurosci. Lett. 134:191-194(1992).
 CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
 CAVA.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR INTERPRO; IPR000981; -.
 DR PFW; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
 Db 1 C 1

Search completed: February 5, 2001, 12:06:02
 Job time: 279 sec

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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:05:38 ; Search time 57.72 Seconds
(without alignments)
8.123 Million cell updates/sec

Title: US-09-687-267-6
Perfect score: 12
Sequence: 1 XXXX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_invertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	9	75.0	6	4 Q08720	Q08720 homo sapien
2	9	75.0	7	2 P70804	P70804 azotobacter
3	9	75.0	7	11 O55184	O55184 rattus norv
4	9	75.0	7	12 Q66113	Q66113 cherry leaf
5	9	75.0	7	12 Q67113	Q67113 influenza a
6	9	75.0	7	12 Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	12 Q9YIR0	Q9YIR0 human adeno
8	9	75.0	7	12 Q9YIO9	Q9YIO9 human adeno
9	9	75.0	7	13 Q42564	Q42564 fugu rubrip
10	9	75.0	8	2 O32560	O32560 escherichia
11	9	75.0	8	4 Q15888	Q15888 homo sapien
12	9	75.0	8	4 Q15890	Q15890 homo sapien
13	9	75.0	8	4 Q15900	Q15900 homo sapien
14	9	75.0	8	4 Q9Y4X6	Q9Y4X6 homo sapien
15	9	75.0	8	6 O02831	O02831 oryctolagus
16	9	75.0	8	6 Q9TRY3	Q9TRY3 sus sp. ins
17	9	75.0	8	10 Q9SAY7	Q9SAY7 dioscorea t
18	9	75.0	8	11 P70243	P70243 mus musculu
19	9	75.0	8	11 O35835	O35835 rattus norv

20	9	75.0	8	12 Q85562	Q85562 moloney mur
21	9	75.0	8	13 Q90493	Q90493 eopsaltria
22	9	75.0	8	13 Q90498	Q90498 erythrura g
23	9	75.0	8	13 Q91098	Q91098 manorina me
24	9	75.0	9	2 Q47063	Q47063 escherichia
25	9	75.0	9	4 Q15999	Q15999 homo sapien
26	9	75.0	9	4 Q99887	Q99887 homo sapien
27	9	75.0	9	6 Q9XT05	Q9XT05 macropus ru
28	9	75.0	9	6 Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9 Q38340	Q38340 lactococcus
30	9	75.0	9	11 Q9QZAB	Q9QZAB mus musculu
31	9	75.0	9	11 P97889	P97889 rattus norv
32	9	75.0	9	12 Q69473	Q69473 human herpe
33	9	75.0	9	12 O12096	O12096 caprine art
34	9	75.0	9	12 O12098	O12098 caprine art
35	9	75.0	9	12 O12100	O12100 caprine art
36	9	75.0	9	12 O12102	O12102 caprine art
37	9	75.0	9	12 O12104	O12104 caprine art
38	9	75.0	9	12 Q90350	Q90350 hepatitis g
39	9	75.0	10	2 Q50032	Q50032 mycobacteri
40	9	75.0	10	2 Q47475	Q47475 escherichia
41	9	75.0	10	2 Q48469	Q48469 klebsiella
42	9	75.0	10	2 Q9K343	Q9K343 escherichia
43	9	75.0	10	3 Q9UWV2	Q9UWV2 schizophyll
44	9	75.0	10	4 Q13318	Q13318 homo sapien
45	9	75.0	10	4 Q9UN90	Q9UN90 homo sapien

ALIGNMENTS

RESULT 1

Q08720 PRELIMINARY; PRT; 6 AA.

AC Q08720; PRELIMINARY; PRT; 6 AA.

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE Y PROTEIN (FRAGMENT).

GN CREB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93010691; PubMed=1396344;

RA Waeber G., Habener J.F.;

RT "Novel testis germ cell-specific transcript of the CREB gene contains an alternatively spliced exon with multiple in-frame stop codons.";

RL Endocrinology 131:2010-2015(1992).

DR EMBL; X68994; CAA48780.1; -.

FT NON_TER 1 1

FT NON_TER 6 6

SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
Db 4 C 4

RESULT 2

P70804 PRELIMINARY; PRT; 7 AA.

ID P70804; PRELIMINARY; PRT; 7 AA.

AC P70804;

DT 01-FEB-1997 (TReMBLrel. 02, Created)

DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE ALGG GENE (FRAGMENT).
GN ALGT.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E.
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 1 C 1

RESULT 3
O55184 PRELIMINARY; PRT; 7 AA.
AC O55184;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299786; PubMed=86611150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
RT expression and chromosomal localization of the human gene";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 3 C 3

RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.
ID Q66113;
AC Q66113;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).
OS cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RA Borja M.;
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain)";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
KW Repeat.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 4 C 4

RESULT 5
Q67113 PRELIMINARY; PRT; 7 AA.
ID Q67113;
AC Q67113;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
KW Hemagglutinin.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 3 C 3

```
Query Match          75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC	Tetraodontidae; Takifugu.
ON	NCBI_TaxID=31033;
OX	[1]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=97442476; PubMed=9295353;
FA	Plummer N.W., McBurney M.W., Meisler M.H.;
RT	"Alternative splicing of the sodium channel SCN8A predicts a truncated
RT	two-domain protein in fetal brain and non-neuronal cells.";
RL	J. Biol. Chem. 272:24008-24015(1997).
DR	EMBL; U97673; AAB80916.1; --
KW	ionic channel.
FT	1.
SQ	SEQUENCE 7 AA; 730 MW; 75B7EA2C73772A0 CRC64;

```

Query match      75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 C 4
Db       5 C 5

RESULT 10
O32560
ID O32560 PRELIMINARY; PRT; 8 AA.
AC O32560;
DT 01-JAN-1998 (TReMBLrel. 05, Created)

```

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
GN PROPIONATE KINASE (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=W3110;
RC Hesslinger C., Sawers G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ001620; CAA04875.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 6 C 6
RESULT 11
Q15888 PRELIMINARY; PRT; 8 AA.
ID Q15888:
AC Q15888:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP15H8A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32069; AAA73878.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB580763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 5 C 5
RESULT 12
Q15890 PRELIMINARY; PRT; 8 AA.
ID Q15890:
AC Q15890:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)

DE (CLONE XP19G12A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32083; AAA73880.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 4 C 4
RESULT 13
Q15900 PRELIMINARY; PRT; 8 AA.
ID Q15900:
AC Q15900:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE (CLONE XP7B11A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
RA Caskey C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32079; AAA73890.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
DB 2 C 2
RESULT 14
Q1594X6 PRELIMINARY; PRT; 8 AA.
ID Q1594X6:
AC Q1594X6:
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE NUCLEAR LIM INTERACTOR (FRAGMENT).
GN NLI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA Schroth A., Bodem J., Royer-Pokora B.;
RT "Genomic structure, alternative transcripts and chromosomal
RT localization of the human LIM domain binding protein 1 gene
RT LDB1/NLI.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243097; CAB45408.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 767 MW; EE6EBDBDEB862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 5 C 5

RESULT 15
002831
ID 002831 PRELIMINARY; PRT; 8 AA.
AC 002831;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; Pubmed=8783186;
RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
RT of full-thickness defects of articular cartilage.";
RL Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
Db 4 C 4

Search completed: February 5, 2001, 12:05:38
Job time: 289 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2001, 11:55:13 ; Search time 42.35 seconds
(without alignments)
3.230 Million cell updates/sec

Title: US-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	P10301	Sequence which cor
2	9	75.0	3	P30982	Binding receptor w
3	9	75.0	3	P91660	Synthetic peptide
4	9	75.0	3	R34022	Metal trapping pep
5	9	75.0	3	R34023	Metal trapping pep
6	9	75.0	3	R51439	IGF-1 analogue N-t
7	9	75.0	3	R51440	IGF-1 analogue N-t
8	9	75.0	3	R51441	IGF-1 analogue N-t
9	9	75.0	3	W19847	Human interleukin-
10	9	75.0	3	W56231	Anti-inflammatory
11	9	75.0	3	W56211	Anti-inflammatory
12	9	75.0	3	W56200	Anti-inflammatory

13	9	75.0	3	19	W56172	Anti-inflammatory
14	9	75.0	3	20	W88037	Peptide used in th
15	9	75.0	3	21	W51896	Biostat in T1232 sy
16	9	75.0	4	2	P10138	Sequence of antiin
17	9	75.0	4	2	P10093	Sequence of peptid
18	9	75.0	4	2	P10382	Enkephalin-like an
19	9	75.0	4	3	P20217	Analgesic and neur
20	9	75.0	4	4	P30083	Sequence of chromo
21	9	75.0	4	4	P30085	Sequence of chromo
22	9	75.0	4	5	P40538	Sequence of cyclic
23	9	75.0	4	5	P40539	Sequence of cyclic
24	9	75.0	4	8	P70833	Sequence encoded b
25	9	75.0	4	10	P91661	Synthetic peptide
26	9	75.0	4	12	R11077	Peptide fragment #
27	9	75.0	4	12	R11079	Peptide fragment #
28	9	75.0	4	12	R11508	Thioredoxin active
29	9	75.0	4	12	R11744	Cyclic platelet ag
30	9	75.0	4	12	R11745	Cyclic platelet ag
31	9	75.0	4	12	R12554	Ocular pressure re
32	9	75.0	4	12	R13935	Antibiotic FR90137
33	9	75.0	4	12	R14723	Farnesyl-protein t
34	9	75.0	4	12	R15751	Farnesyl-protein t
35	9	75.0	4	12	R15752	Farnesyl-protein t
36	9	75.0	4	12	R15753	Farnesyl-protein t
37	9	75.0	4	12	R15754	Farnesyl-protein t
38	9	75.0	4	12	R15755	Farnesyl-protein t
39	9	75.0	4	12	R15756	Farnesyl-protein t
40	9	75.0	4	12	R15757	Farnesyl-protein t
41	9	75.0	4	12	R15758	Farnesyl-protein t
42	9	75.0	4	12	R15759	Farnesyl-protein t
43	9	75.0	4	12	R15760	Farnesyl-protein t
44	9	75.0	4	12	R15761	Farnesyl-protein t
45	9	75.0	4	21	Y80840	Fluorophore-label

ALIGNMENTS

RESULT 1

P10301

ID P10301 standard; Protein; 3 AA.

XX

XX P10301;

XX

DT 19-AUG-1992 (first entry)

XX

DE Sequence which corresp. to residues 19-21 of insulin A chain.

XX

KW Cystine peptide; insulin activity; hormone; diabetes therapy;

KW antidiabetic agent.

XX

OS Mammal.

XX

FF Key Location/Qualifiers

FT Disulfide-bond 2

FT /note= "bonded to Cys(5) of P10115, which is

FT residue 19 of the B chain fragment

FT B15-27"

XX

XX DD147942-A.

XX

PD 29-APR-1981.

XX

PF 01-FEB-1980; 80DD-0011868.

XX

PR 20-AUG-1979; 79DD-0215100.

XX

PA (LOSS/) LOSSE G.

XX

XX IGF-1 analogue N-t

XX IGF-1 analogue N-t

XX Human interleukin-

XX Anti-inflammatory

XX Anti-inflammatory

XX WPI; 1981-53498D/30 (53498D).

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments
PT of insulin A and B chains
XX
PS Claim 1; Page 10; 11pp; German.
XX
CC The inventors claim the prepn. of new cysteine peptides with insulin-
CC like activity. The new peptides comprise a sequence with corresp. to
CC a central portion of the insulin B chain (esp. B15-27) and a
CC cysteine-contg. peptide with an AA sequence corresp. to a terminal
CC portion of the insulin A chain (esp. A1-7). The new cysteine
CC peptides are antidiabetic agents with appreciable insulin activity
CC (lower than that of insulin itself) and low antigenic activity.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 2 C 2

RESULT 2
P90982 ID P90982 standard; peptide; 3 AA.
XX AC P90982;
XX
DT 06-JUN-1990 (first entry)
XX
DE Binding receptor with selectivity for a target ligand, borne by
DE an article for inactivating toxic materials.
XX
KW Toxic material; inactivator; organophosphorous cpds.; nerve poison;
KW pesticide; decontaminant; military.
XX
PN WO8902920-A.
XX
PD 06-APR-1989.
XX
PF 04-OCT-1988; 88WO-US03422.
XX
PR 05-OCT-1987; 87US-0105312.
XX
PA (LITT) LITTLE AD INC.
XX
PI Taylor RF;
XX
DR WPI; 1989-114395/15.
XX
PT Article for inactivating toxic materials, eg organo:phosphorous cpds. -
PT comprises solid carrier bearing target ligand binding receptor
PT and ligand-degrading receptor, pref. enzyme
XX
PS Claim 7a; page 42; 57pp; English.
XX
CC The article for inactivating a toxic material comprises a solid carrier
CC bearing a first receptor which binds the target ligand and a second
CC receptor which degrades the target ligand. This synthetic peptide is
CC a preferred first receptor. The article may be used for covering
CC surfaces to protect or decontaminate the surface. The article is esp. for
CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg
CC pesticides and nerve poisons, bacteria and viruses, in environmental,
XX chemical, military and industrial settings.
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;

QY 1 C 1
DB 3 C 3

RESULT 4
R34022 ID R34022 standard; peptide; 3 AA.
XX AC R34022;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 2 C 2

RESULT 3
P91660 ID P91660 standard; protein; 3 AA.
XX AC P91660;
XX
DT 29-JUN-1990 (first entry)
XX
DE Synthetic peptide corresp. to residues 12-14 of naturally occurring
DE epidermal growth factor (EGF).
XX
KW Epidermal growth factor; angiogenesis; synthetic peptide.
XX
FH Key : Location/Qualifiers
FT Misc-difference 1 :./label=OTHER
FT :./label="H-Gly"
FT Misc-difference 3 /note="H-Gly"
FT :label=OTHER
FT /note="(aceto amido methyl) NH2-Cys"
XX
PN WO8901489-A.
XX
PD 23-FEB-1989.
XX
PF 10-AUG-1988; 88WO-AU00300.
XX
PR 10-AUG-1987; 87AU-0003629.
XX
PA (CSIR) COMMONWEALTH SCIENT ORG.
XX
PI McAuslan BR;
XX
DR WPI; 1989-068852/09.
XX
PT Synthetic peptide active in stimulating angiogenesis -
PT has sequences corresponding to amino acid sequences occurring in
PT epidermal growth factor.
XX
PS Claim 3; page 10; 11pp; English.
XX
CC The inventors claim synthetic peptides which correspond to sequences
CC occurring in EGF, but excluding EGF. The peptides are angiogenic
CC and have corresp. applications, eg for the healing of wounds and
CC burns. Their relative shortness means that they pose fewer synthesis
CC problems than the entire EGF molecule. They can be admin. singly or
CC association with each other or in association with an angiogenic
CC stimulator.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 4
R34022 ID R34022 standard; peptide; 3 AA.
XX AC R34022;

XX 19-MAY-1993 (first entry)
 DT Metal trapping peptide intermediate.
 DE Electrostatic interaction; metalloprotein; binding site;
 KW protecting group.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "Boc protected"
 DE Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH
 FT of cysteine"
 FT Modified-site 3 /note= "OME protected"
 FT
 FT JP04346999-A.
 PN 02-DEC-1992.
 PD 24-MAY-1991; 91JP-0120196.
 XX 24-MAY-1991; 91JP-0120196.
 XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
 PA WPI; 1993-021449/03.
 DR New acyclic peptide with metal trapping activity - exhibits in
 XX vivo metal transporting action and can be used as drug,
 FT diagnostic agent or functional material
 FT Claim 3; Page 2; 9pp; Japanese.
 PS The acyclic peptide (see R31340) with metal trapping activity may be
 CC produced by fragment condensation using the peptide fragments given in
 CC R34022-29.
 CC Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 14; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
 Db 2 C 2

RESULT 5
 R34023
 ID R34023 standard; peptide; 3 AA.
 XX
 AC R34023;
 XX
 DT 19-MAY-1993 (first entry)
 XX Metal trapping peptide intermediate.
 DE Electrostatic interaction; metalloprotein; binding site;
 KW protecting group.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "HCl.H-Val"
 FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH

FT Modified-site 3 of cysteine"
 FT /note= "OME protected"
 XX JP04346999-A.
 PN 02-DEC-1992.
 PD 24-MAY-1991; 91JP-0120196.
 XX 24-MAY-1991; 91JP-0120196.
 XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
 PA WPI; 1993-021449/03.
 DR New acyclic peptide with metal trapping activity - exhibits in
 XX vivo metal transporting action and can be used as drug,
 FT diagnostic agent or functional material
 FT Claim 3; Page 2; 9pp; Japanese.
 PS The acyclic peptide (see R31340) with metal trapping activity may be
 CC produced by fragment condensation using the peptide fragments given in
 CC R34022-29.
 CC Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 14; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
 Db 2 C 2

RESULT 6
 R51439
 ID R51439 standard; peptide; 3 AA.
 XX
 AC R51439;
 XX
 DT 27-OCT-1994 (first entry)
 XX IGF-1 analogue N-terminal.
 DE Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 KW Homo sapiens.
 XX
 OS WO9406445-A.
 PN 31-MAR-1994.
 PD 02-SEP-1993; 93WO-US08279.
 XX 17-SEP-1992; 92US-0947035.
 XX (EMBR-) EMBREX INC.
 PA (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 XX WPI; 1994-118144/14.
 DR Increasing growth of birds - with insulin-like growth factor
 PT delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.

XX Claim 6; Page 37; 45pp; English.
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3
 CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 3 C 3

RESULT 7
 R51440
 ID R51440 standard; peptide; 3 AA.
 AC R51440;
 XX
 XX 27-OCT-1994 (first entry)
 DE IGF-1 analogue N-terminal.
 XX
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 XX
 XX Homo sapiens.
 OS
 XX WO9406445-A.
 PN
 XX 31-MAR-1994.
 PD
 XX 02-SEP-1993; 93WO-US08279.
 PF
 XX 17-SEP-1992; 92US-0947035.
 PR
 XX (EMBR-) EMBREX INC.
 PA (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX
 XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 PI WPI; 1994-118144/14.
 DR
 XX Increasing growth of birds - with insulin-like growth factor
 PT delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.
 XX
 XX Claim 6; Page 37; 45pp; English.
 PS
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 3 C 3

RESULT 8
 R51441
 ID R51441 standard; peptide; 3 AA.
 XX
 AC R51441;
 XX
 XX 27-OCT-1994 (first entry)
 DE IGF-1 analogue N-terminal.
 XX
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 XX
 XX Homo sapiens.
 OS
 XX WO9406445-A.
 PN
 XX 31-MAR-1994.
 PD
 XX 02-SEP-1993; 93WO-US08279.
 PF
 XX 17-SEP-1992; 92US-0947035.
 PR
 XX (EMBR-) EMBREX INC.
 PA (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX
 XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 PI WPI; 1994-118144/14.
 DR
 XX Increasing growth of birds - with insulin-like growth factor
 PT delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.
 XX
 XX Claim 6; Page 37; 45pp; English.
 PS
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3
 CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Ieu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 3 c 3

RESULT 9

W19847
 ID W19847 standard; Peptide; 3 AA.

XX AC W19847;

XX DT 23-SEP-1997 (first entry)

XX DE Human interleukin-12 p40 subunit N-terminal peptide.

XX KW Interleukin-12; Fc gamma-1; immunosuppressive; autoimmune disease;
 XX KW graft rejection; toxic shock; therapy.

XX OS Homo sapiens.

XX PN WO9720062-A1.

XX PD 05-JUN-1997.

XX PF 02-DEC-1996; 96WO-US19181.

XX PR 01-DEC-1995; 95US-0565856.

XX PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX PA (UYMA-) UNIV MASSACHUSETTS.

XX PI Steel AW, Strom TB;

XX DR WPI; 1997-310615/28.

XX DR N-PSDB; T72095-96.

XX PT Fusion protein containing interleukin-12 p40 sub-unit - has
 PT increased stability, used to inhibit graft rejection, or treat
 PT autoimmune disease and endotoxin-induced shock

XX PS Example; Fig 2; 36pp; English.

XX CC A peptide (W19847) comprises the three N-terminal amino acid
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is
 CC encoded both by native human p40 cDNA (T72096) and by a primer
 CC (T72095), based on the native sequence. PCR amplification has
 CC been used to amplify p40 cDNA. A fusion protein comprising the
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed
 CC in E. coli. This fusion protein has a longer in vivo half-life
 CC than native p40 and can be used as an immunosuppressive (e.g. to
 CC treat autoimmune diseases or to inhibit graft rejection) or to
 CC treat or prevent endotoxin-induced shock.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 2 c 2

RESULT 10

W56231
 ID W56231 standard; peptide; 3 AA.

XX AC W56231;

XX DT 20-JUL-1998 (first entry)

XX DE Anti-inflammatory tripeptide.

XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
 XX KW T-cell inhibitory activity; adherence; extracellular matrix;
 XX KW up-regulation; fas receptor expression; inflammation.

XX OS Synthetic.

XX PN WO9809985-A2.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-IL00295.

XX PR 28-MAY-1997; 97US-0864301.

XX PR 03-SEP-1996; 96US-0025376.

XX PR 20-NOV-1996; 96US-0753141.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX DR WPI; 1998-193550/17.

XX PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX PS Claim 7; Page 35; 42pp; English.

XX CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:

CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

CC Xaa = any amino acid residue.

CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 C 1

Db 3 c 3

RESULT 11
W56211
ID W56211 standard; peptide; 3 AA.

XX AC W56211;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.

XX OS Synthetic.

XX PN W09809985-A2.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-IL00295.

XX PR 28-MAY-1997; 97US-0864301.

XX PR 03-SEP-1996; 96US-0025376.

XX PR 20-NOV-1996; 96US-0753141.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX WPI; 1998-193550/17.

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.

XX PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,

XX PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX PS Claim 6; Page 35; 42pp; English.

XX W56171-248 represent anti-inflammatory tripeptides of the invention.

XX CC They are derived from the formulae:

XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

XX CC Xaa = any amino acid residue.

XX CC Cyclic derivatives of the peptides also function as anti-inflammatory

XX CC agents. The peptides can be covalently linked to one another either

XX CC directly or through a spacer. The peptides and their derivatives have

XX CC macrophage inhibitory and T-cell inhibitory activity and thus,

XX CC anti-inflammatory activity. The peptides and compositions have

XX CC anti-immune activity, i.e. inhibitory effects against a cellular and

XX CC humoral immune response, including a response not associated with

XX CC inflammation. The peptides also inhibit the ability of macrophages and

XX CC T-cells to adhere to extracellular matrix components and fibronectin, as

XX CC well as up-regulated fas receptor expression in T-cells. They can be used

XX CC to inhibit unwanted immune reaction and inflammation.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 12
W56200
ID W56200 standard; peptide; 3 AA.

XX AC W56200;
XX DT 20-JUL-1998 (first entry)

XX Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.

XX OS Synthetic.

XX PN W09809985-A2.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-IL00295.

XX PR 28-MAY-1997; 97US-0864301.

XX PR 03-SEP-1996; 96US-0025376.

XX PR 20-NOV-1996; 96US-0753141.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX WPI; 1998-193550/17.

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.

XX PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,

XX PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX PS Claim 6; Page 35; 42pp; English.

XX W56171-248 represent anti-inflammatory tripeptides of the invention.

XX CC They are derived from the formulae:

XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

XX CC Xaa = any amino acid residue.

XX CC Cyclic derivatives of the peptides also function as anti-inflammatory

XX CC agents. The peptides can be covalently linked to one another either

XX CC directly or through a spacer. The peptides and their derivatives have

XX CC macrophage inhibitory and T-cell inhibitory activity and thus,

XX CC anti-inflammatory activity. The peptides and compositions have

XX CC anti-immune activity, i.e. inhibitory effects against a cellular and

XX CC humoral immune response, including a response not associated with

XX CC inflammation. The peptides also inhibit the ability of macrophages and

XX CC T-cells to adhere to extracellular matrix components and fibronectin, as

XX CC well as up-regulated fas receptor expression in T-cells. They can be used

XX CC to inhibit unwanted immune reaction and inflammation.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 13
W56172
ID W56172 standard; peptide; 3 AA.

XX AC W56172;
XX DT 20-JUL-1998 (first entry)

XX Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.

XX OS Synthetic.

XX PN W09809985-A2.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-IL00295.

XX PR 28-MAY-1997; 97US-0864301.

XX PR 03-SEP-1996; 96US-0025376.

XX PR 20-NOV-1996; 96US-0753141.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX WPI; 1998-193550/17.

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.

XX PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,

XX PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX PS Claim 5; Page 34; 42pp; English.

XX W56171-248 represent anti-inflammatory tripeptides of the invention.

XX CC They are derived from the formulae:

XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

XX CC Xaa = any amino acid residue.

XX CC Cyclic derivatives of the peptides also function as anti-inflammatory

XX CC agents. The peptides can be covalently linked to one another either

XX CC directly or through a spacer. The peptides and their derivatives have

XX CC macrophage inhibitory and T-cell inhibitory activity and thus,

XX CC anti-inflammatory activity. The peptides and compositions have

XX CC anti-immune activity, i.e. inhibitory effects against a cellular and

XX CC humoral immune response, including a response not associated with

XX CC inflammation. The peptides also inhibit the ability of macrophages and

XX CC T-cells to adhere to extracellular matrix components and fibronectin, as

XX CC well as up-regulated fas receptor expression in T-cells. They can be used

XX CC to inhibit unwanted immune reaction and inflammation.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 13
W56172
ID W56172 standard; peptide; 3 AA.

XX AC W56172;
XX DT 20-JUL-1998 (first entry)

XX Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
XX KW T-cell inhibitory activity; adherence; extracellular matrix;
XX KW up-regulation; fas receptor expression; inflammation.

XX OS Synthetic.

XX PN W09809985-A2.

XX PD 12-MAR-1998.

XX PF 03-SEP-1997; 97WO-IL00295.

XX PR 28-MAY-1997; 97US-0864301.

XX PR 03-SEP-1996; 96US-0025376.

XX PR 20-NOV-1996; 96US-0753141.

XX PA (YEDA) YEDA RES & DEV CO LTD.

XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;

XX WPI; 1998-193550/17.

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.

XX PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,

XX PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX PS Claim 5; Page 34; 42pp; English.

XX W56171-248 represent anti-inflammatory tripeptides of the invention.

XX CC They are derived from the formulae:

XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where

XX CC Xaa = any amino acid residue.

XX CC Cyclic derivatives of the peptides also function as anti-inflammatory

XX CC agents. The peptides can be covalently linked to one another either

XX CC directly or through a spacer. The peptides and their derivatives have

XX CC macrophage inhibitory and T-cell inhibitory activity and thus,

XX CC anti-inflammatory activity. The peptides and compositions have

XX CC anti-immune activity, i.e. inhibitory effects against a cellular and

XX CC humoral immune response, including a response not associated with

XX CC inflammation. The peptides also inhibit the ability of macrophages and

XX CC T-cells to adhere to extracellular matrix components and fibronectin, as

XX CC well as up-regulated fas receptor expression in T-cells. They can be used

XX CC to inhibit unwanted immune reaction and inflammation.

XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

OS Synthetic.
 PN WO9809985-A2.
 XX
 PD 12-MAR-1998.
 XX
 PF 03-SEP-1997; 97WO-IL00295.
 XX
 XX 28-MAY-1997; 97US-0864301.
 PR 03-SEP-1996; 96US-0025376.
 PR 20-NOV-1996; 96US-0753141.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
 XX
 XX WPI; 1998-193550/17.
 XX
 XX Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease
 XX
 XX Claim 3; Page 34; 42pp; English.
 XX
 CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
 CC Xaa = any amino acid residue.
 CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.
 XX
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 1 C 1

RESULT 14
 W88037
 ID W88037 standard; peptide; 3 AA.
 XX
 AC W88037;
 XX
 DT 09-APR-1999 (first entry)
 XX
 DE Peptide used in the hair composition of the invention.
 XX
 KW Hair; styling; wave.
 XX
 XX Synthetic.
 OS
 XX JP11012138-A.
 PN
 XX 19-JAN-1999.
 PD
 XX 18-JUN-1997; 97JP-0161657.
 PF
 XX

PR 18-JUN-1997; 97JP-0161657.
 XX (LIOY) LION CORP.
 XX
 XX WPI; 1999-148442/13.
 XX
 XX New composition for hair - comprises oligopeptide having more than 2
 PT cysteine residues and reducing agent
 XX
 XX Example 2; Page 6; 17pp; Japanese.
 PS
 XX Peptides W88033-39 are used in the hair composition of the invention.
 CC The specification describes a hair composition that comprises at
 CC least one oligopeptide having more than two cysteine residues and more
 CC than three amino acid residues of the same kind (except cysteine) and a
 CC reducing agent. The composition is useful for styling hair to take
 CC various shapes and waves safely and effectively.
 XX
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 20; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 1 C 1

RESULT 15
 Y51896
 ID Y51896 standard; peptide; 3 AA.
 XX
 AC Y51896;
 XX
 DT 16-JUN-2000 (first entry)
 XX
 DE Biostatin TT232, synthesising peptide 1.
 XX
 KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;
 KW cellular proliferation inhibition; somatostatin; antitumor.
 XX
 XX Unidentified.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 2 /note= "TFA*Lys(2)"
 FT Modified-site 3 /note= "Cys(Acm)"
 FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"
 XX
 PN WO200011032-A2
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-EP06131.
 XX
 PR 20-AUG-1998; 98WO-EP05306.
 XX
 PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.
 XX
 PI Braum G, Lifferth A, Birr C;
 XX
 XX WPI; 2000-224663/19.
 XX
 XX Biostatin preparation in high yield by solid synthesis, including
 PT closure of disulfide bridge before cleavage from support, useful as
 PT antitumor agent
 XX
 XX Example 4; Page 23; 33pp; German.
 PS
 XX

CC This invention describes a novel method for the solid phase (SP)
 CC synthesis of biostatin (PT 232) (I) which includes closing the disulfide
 CC bridge by oxidation of the completely or partially constructed peptide
 CC while still bonded to the solid phase. The products of the invention have
 CC cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits the
 CC tyrosine kinase activity of various human stomach cancer cell lines and
 CC thus inhibits cellular proliferation. The heptapeptide (I) described in
 CC the invention is a somatostatin analog which shows strong antitumor
 CC activity in vitro and in vivo. The SP synthesis method gives (I) is more
 CC easily and in markedly higher yield than by the method of EP505680, in
 CC which the cyclization is carried out after cleaving the peptide from the
 CC resin. The solution method is also a simple synthesis of (I) in high
 CC yield; typically the tert-butyl-protected precursor can be oxidized in
 CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the
 CC synthesis of biostatin PT232 described in the method of the invention.

XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
 Db 2 c 2

Search completed: February 5, 2001, 12:01:19
 Job time: 366 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 11:56:18 ; Search time 30.91 Seconds
(without alignments)
2.324 Million cell updates/sec

Title: us-09-687-267-1
Perfect score: 12
Sequence: 1 CXXX 4
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/6_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-386-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-397-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	3	1	US-07-791-213D-22
22	9	75.0	3	1	US-07-791-213D-38
23	9	75.0	3	1	US-07-945-982-2
24	9	75.0	3	1	US-07-945-982-8
25	9	75.0	3	1	US-07-947-035-3
26	9	75.0	3	1	US-07-947-035-4
27	9	75.0	3	1	US-07-947-035-5
28	9	75.0	3	1	US-08-285-443-4

29 9 75.0 3 1 US-08-079-812-31 Sequence 31, Appl
30 9 75.0 3 1 US-08-122-510-11 Sequence 11, Appl
31 9 75.0 3 1 US-08-122-510-12 Sequence 12, Appl
32 9 75.0 3 1 US-08-122-510-13 Sequence 13, Appl
33 9 75.0 3 1 US-07-789-913-26 Sequence 26, Appl
34 9 75.0 3 1 US-08-371-930-4 Sequence 4, Appl
35 9 75.0 3 1 US-08-049-794-26 Sequence 26, Appl
36 9 75.0 3 1 US-08-372-455-2 Sequence 2, Appl
37 9 75.0 3 1 US-08-372-455-8 Sequence 8, Appl
38 9 75.0 3 1 US-08-321-585A-1 Sequence 1, Appl
39 9 75.0 3 1 US-08-321-585A-2 Sequence 2, Appl
40 9 75.0 3 1 US-08-321-585A-3 Sequence 3, Appl
41 9 75.0 3 1 US-08-446-908-14 Sequence 14, Appl
42 9 75.0 3 1 US-08-231-205A-14 Sequence 14, Appl
43 9 75.0 3 1 US-08-293-150A-22 Sequence 22, Appl
44 9 75.0 3 1 US-08-293-150A-38 Sequence 38, Appl
45 9 75.0 3 3 US-08-447-515-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-07-791-213D-23
; Sequence 23, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,507
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 2
US-07-791-213D-39
; Sequence 39, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791.213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-39

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 3
US-08-133-804-9
; Sequence 9, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-133-804-9

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 4
US-08-354-240A-12
; Sequence 12, Application US/08354240A
; Patent No. 5670356
; GENERAL INFORMATION:
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Wood, Keith V.
; TITLE OF INVENTION: MODIFIED LUCIFERASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1514
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,240A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435

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; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 5
US-08-461-838-9
; Sequence 9, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (ser-Cys)"
; US-08-461-838-9

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 6
US-08-293-150A-23
; Sequence 23, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 7
US-08-293-150A-39
; Sequence 39, Application US/08293150A
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; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 8
US-08-461-386-9
; Sequence 9, Application US/08/461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..2
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 9
US-08-465-380-307
; Sequence 307, Application US/08/465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/268
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

RESULT 10
US-08-486-397-307
;; Sequence 307, Application US/08486397
;; Patent No. 5866542
;; GENERAL INFORMATION:
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
;; APPLICANT: Peter W. Bergum
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
;; NUMBER OF SEQUENCES: 357
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,397
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/269
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

RESULT 11
US-08-486-399-307
;; Sequence 307, Application US/08486399
;; Patent No. 5866543
;; GENERAL INFORMATION:
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
;; APPLICANT: Peter W. Bergum
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
;; NUMBER OF SEQUENCES: 356
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,399
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/270
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 1 C 1

RESULT 12

US-08-461-965-307
; Sequence 307, Application US/08461965
; Patent No. 5872098

GENERAL INFORMATION:

; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 307:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 1 C 1

RESULT 13

US-08-634-641-307
; Sequence 307, Application US/08634641
; Patent No. 5955294

GENERAL INFORMATION:

; APPLICANT: Vlasuk, George P. Vlasuk
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Mensens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,641
; FILING DATE: April 19, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 307:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

RESULT 14

US-08-818-253-52
; Sequence 52, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

RESULT 15

US-09-249-471-307
; Sequence 307, Application US/09249471
; Patent No. 6040441
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Larocche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemaus, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berigum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,471
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; OTHER INFORMATION: amino acid.
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

Search completed: February 5, 2001, 12:01:53
Job time: 335 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 11:57:43 ; Search time 34.92 Seconds
(without alignments)
7.778 Million cell updates/sec

Title: US-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.66.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	A22565	R-phycoerythrin al
2	9	75.0	4	I51049	metallothionein-A
3	9	75.0	4	S43959	Ig mu chain V regi
4	9	75.0	4	S52238	pallidipin - assas
5	9	75.0	5	A22565	R-phycoerythrin al
6	9	75.0	5	F22565	R-phycoerythrin ga
7	9	75.0	5	A33882	cadmium-binding pe
8	9	75.0	5	B45525	actin I - malaria
9	9	75.0	5	S65726	hemoglobin, extrac
10	9	75.0	6	JU0355	lipopeptide WS1279
11	9	75.0	6	C22565	R-phycoerythrin be
12	9	75.0	6	I37027	protamine P1 - gor
13	9	75.0	6	I37263	Y protein - human
14	9	75.0	6	S29881	Na+/K+-exchanging
15	9	75.0	6	H48394	glycoprotein compo
16	9	75.0	6	I67345	MHC H2-K-k cell su
17	9	75.0	6	I65546	MHC H2-L antigen -
18	9	75.0	6	PT0652	T-cell receptor be
19	9	75.0	6	F41946	T-cell receptor ga
20	9	75.0	6	I49421	laminin B1 - weste
21	9	75.0	6	I79564	hypothetical TCl3
22	9	75.0	7	PH1408	Ig heavy chain V r
23	9	75.0	7	A58512	venom heptapeptide
24	9	75.0	7	S08606	hypothetical prote
25	9	75.0	7	S38516	mablinin II chain
26	9	75.0	7	B34818	vicilin 57K chain
27	9	75.0	7	B33882	cadmium-binding he
28	9	75.0	7	A34026	acetylcholinestera
29	9	75.0	7	A12016	formylglycinamide

30 9 75.0 7 2 PH1602 Ig H chain V-D-J r
31 9 75.0 7 2 PH0932 T-cell receptor be
32 7 4 I56695 hypothetical L2 pr
33 9 75.0 8 2 PH1407 Ig heavy chain V r
34 9 75.0 8 2 S59622 metallothionein is
35 9 75.0 8 2 XGHUEU urine glycopeptide
36 9 75.0 8 2 A25836 L-serine dehydrata
37 9 75.0 8 2 PC1002 leucine--trNA liga
38 9 75.0 8 2 S19288 acylase - Kluyvera
39 9 75.0 8 2 A37521 R-phycoerythrin ga
40 9 75.0 8 2 C61512 variant surface gl
41 9 75.0 8 2 D61512 variant surface gl
42 9 75.0 8 2 PH1618 Ig H chain V-D-J r
43 9 75.0 8 2 PH0803 T-cell receptor al
44 9 75.0 8 2 I57018 gene Cfr protein
45 9 75.0 8 2 PH0934 T-cell receptor be

ALIGNMENTS

RESULT 1
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 2
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)
A:Reference number: I51049; MUID:95324545
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 4 C 4

RESULT 3
S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 2 C 2

RESULT 4
S5238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S55238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuning
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib
A:Reference number: S55238; MUID:95251610
A:Accession: S55238
A:Molecule type: protein
A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 3 C 3

RESULT 5
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 2 C 2

RESULT 6
F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: F22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 3 C 3

RESULT 7
A33882
cadmium-binding pentapeptide - downy thornapple
C:Species: Datura innoxia (downy thornapple)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C:Accession: A33882
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan
A:Reference number: A94182; MUID:88016144
A:Accession: A33882
A:Molecule type: protein
A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 2 C 2

RESULT 8
B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: B45525
R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schre
Mol. Biochem. Parasitol. 35, 167-176, 1989
A:Title: Stage-specific expression and genomic organization of the actin genes o
A:Reference number: A45525; MUID:89364996
A:Accession: B45525
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <WES>
A:Cross-references: GB:J03988
A:Note: the authors translated the codon GAA for residue 3 as Gly
C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 4 C 4

RESULT 9
S65726
hemoglobin, extracellular, chain b - earthworm (umbilicus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65726
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A:Reference number: S65721; MUID:96176855
A:Accession: S65726
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 4 C 4

RESULT 10
JU0355
lipopeptide WS1279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JU0355
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin
A:Reference number: JU0355; MUID:91300586
A:Accession: JU0355
A:Molecule type: protein
A:Residues: 1-6 <TSU>
A>Note: the structure was confirmed by synthesis
C:Keywords: blocked amino end; lipoprotein
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 1 C 1

RESULT 11
C22565
R-phycoerythrin beta-1 chain - red alga (Gastroleonium coulteri) (fragment)
C:Species: Gastroleonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 4 C 4

RESULT 12
I37027
protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralto, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: I37013; MUID:94040810
A:Accession: I37027
A>Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 6 C 6

RESULT 13
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waechter, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative
A:Reference number: I37263; MUID:93010691
A:Accession: I37263
A>Status: Preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 4 C 4

RESULT 14
S29881
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S29881
R:Waldnerhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases from
A:Reference number: S29881; MUID:85131201
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney

C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 2 C 2

RESULT 15

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Mathur, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
|
Db 6 C 6

Search completed: February 5, 2001, 12:02:32
Job time: 289 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:23 ; Search time 20.72 seconds
(without alignments)
6.234 Million cell updates/sec

Title: US-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	8	1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8	1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9	1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9	1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9	1 CONO_CONST	P05487 conus stria
6	9	75.0	9	1 DNE1_LOCM1	P16339 locusta mig
7	9	75.0	9	1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9	1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9	1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9	1 OXYA_SQUAC	P42997 squalus aca
11	9	75.0	9	1 OXYF_SCYCA	P42997 scyllorhinu
12	9	75.0	9	1 OXYT_BUFRE	P42995 bufo regula
13	9	75.0	9	1 OXYT_CYPCA	P23879 cyprinus ca
14	9	75.0	9	1 OXYT_EISFO	P42998 eisenia foe
15	9	75.0	9	1 OXYT_OCTUV	P80027 octopus vul
16	9	75.0	9	1 OXYT_RABIT	P32878 oryctolagus
17	9	75.0	9	1 OXYT_RAJCL	P42994 raja clavat
18	9	75.0	9	1 OXYV_SQUAC	P43000 squalus aca
19	9	75.0	9	1 RS11_SALTY	O54296 salmonella
20	9	75.0	9	1 SAP_STOVA	P24047 stomopneute
21	9	75.0	9	1 TAL1_PICUA	P17440 pichia jadi
22	9	75.0	9	1 TAL3_PICUA	P17441 pichia jadi
23	9	75.0	10	1 GLEM_HUMAN	P02728 homo sapien
24	9	75.0	10	1 GON2_CHEPR	P80678 cheilosoma
25	9	75.0	10	1 RCA_PINPS	P81084 pinus pinas
26	9	75.0	12	1 CXAL_CONIM	P50983 conus imper
27	9	75.0	12	1 N040_LOTJA	O22426 lotus japon
28	9	75.0	12	1 N040_SESRO	O24369 sesbania ro
29	9	75.0	12	1 N040_SOYBN	P55960 glycine max
30	9	75.0	12	1 RR16_GINBI	P36207 ginkgo bilo
31	9	75.0	12	1 TAL0_TREME	P01371 tremella me
32	9	75.0	12	1 UR2A_CATCO	P04558 catostomus
33	9	75.0	12	1 UR2B_CATCO	P04559 catostomus

34	9	75.0	12	1 UR2B_CYPCA	P04561 cyprinus ca
35	9	75.0	12	1 UR2_GILMI	P01147 gillichys
36	9	75.0	12	1 UR2_POLSP	P81022 polyodon sp
37	9	75.0	12	1 UR2_SCYCA	P35490 scyllorhinu
38	9	75.0	12	1 YZPY_ECOLI	P17776 escherichia
39	9	75.0	13	1 ACT7_SOYBN	P15987 glycine max
40	9	75.0	13	1 CXAL_CONST	P15471 conus stria
41	9	75.0	13	1 CXA2_CONGE	P01520 conus geogr
42	9	75.0	13	1 CXAA_CONST	P28878 conus stria
43	9	75.0	13	1 CXET_CONTE	P81755 conus texti
44	9	75.0	13	1 GER1_HORVU	P28525 hordeum vul
45	9	75.0	13	1 GER2_HORVU	P28526 hordeum vul

ALIGNMENTS

RESULT 1
ACT_CARMA
ID ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN (FRAGMENT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 KDA.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC INTERPRO: IPR000279; .
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAEB3 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 2 C 2

RESULT 2
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25P-25P(1971).
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR: A03188; XGHUEU.
KW Glycoprotein.
FT CARBOHYD 1 1 S-LINKED (GAL. .).
SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1EB1E CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 3
CCAP_CARMA STANDARD; PRT; 9 AA.
ID CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CARDIOACTIVE PEPTIDE (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
Tenebrio molitor (Yellow mealworm), and
Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C.MAENAS; TISSUE=PERICARDIAL ORGANS;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.MOLITOR, AND S.ERIDANIA; TISSUE=HEAD;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
INTO THE HEMOLYPH.
DR PIR: A26363; A26363.
DR PIR: S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
MOD_RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 4
CONO_CONGE STANDARD; PRT; 9 AA.
ID CONO_CONGE STANDARD; PRT; 9 AA.
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LYS-CONOPRESSIN G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: A28495; A28495.
DR INTERPRO: IPR000981; .
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
MOD_RES 9 9
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 5
CONO_CONST STANDARD; PRT; 9 AA.
ID CONO_CONST STANDARD; PRT; 9 AA.
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ARG-CONOPRESSIN S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]

RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Oliveira B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: B28495; B28495.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 1 C 1

RESULT 6
 DNFL_LOCM1 STANDARD; PRT; 9 AA.
 AC P16339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 RN [1]
 RP SEQUENCE.

RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;
 RX MEDLINE=88077077; PubMed=3689410;
 RA Proulx J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
 RA Delaage M., Schooley D.A.;
 RT "Identification of an arginine vasopressin-like diuretic hormone from
 RT Locusta migratoria.";
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
 CC -!- FUNCTION: DIURETIC HORMONE.
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR: A29477; A29477.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT DISULFID 1 6
 FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
 FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 1 C 1

RESULT 7
 ISOT_CYPCA STANDARD; PRT; 9 AA.
 ID ISOT_CYPCA
 AC P42993;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE ISOTOCIN.

OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 RN [1]
 RP SEQUENCE.

RC TISSUE=PIUITARY;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony
 RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
 RT water bony fishs.";
 RL Comp. Biochem. Physiol. 14:245-254(1965).

CC -!- FUNCTION: ANTI-DIURETIC HORMONE.

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

PIR: A61364; A61364.

DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.

FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 1 C 1

RESULT 8
 MGMT_BOVIN STANDARD; PRT; 9 AA.
 ID MGMT_BOVIN
 AC P29177;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).
 GN MGMT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE.

RC TISSUE=THYMUS;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B., Hall J., Karren P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 RT methyltransferase.";
 RL Nucleic Acids Res. 18:17-21(1990).
 CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
 CC IRREVERSIBLY INACTIVATED.
 CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN
 CC L-CYSTEINE -> DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-
 CC L-CYSTEINE.

CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
 DR INTERPRO: IPR001497; .

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DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 9 C 9

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN.
OS Scyllorhinus canicula (Spotted dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC 1- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 10
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN (ASPARTOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;

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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val18-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
ID OXYF_SCYCA
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC 1- FUNCTION: DISPLAYS OXYTIC ACTIVITY ON RAT UTERUS.
CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTICIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 12
OXYT_BUFRE

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ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE SERITOCIN.
OS Bufo regularis (African toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae;
OC Bufo.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY NEUROINTERMEDIATE LOBE;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EAS6D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

RESULT 13
OXYT_CYPCA STANDARD; PRT; 9 AA.
ID OXYT_CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE VASOTOCIN.
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C. CARPIO; TISSUE=PITUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. MARINUS; TISSUE=PITUITARY;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): Isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: B61364; B61364.
DR PIR: S06375; S06375.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 1 C 1

RESULT 15
OXYT_OCTVU STANDARD; PRT; 9 AA.
ID OXYT_OCTVU STANDARD; PRT; 9 AA.
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CEPHALOTOCIN.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
RN [1]
RP SEQUENCE.
RC TISSUE=NERVE ENDINGS;

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RX MEDLINE-92270139; PubMed-1589145;
 RA Reich G.;
 RT "A new peptide of the oxytocin/vasopressin family isolated from
 RL nerves of the cephalopod Octopus vulgaris.";
 RL Neurosci. Lett. 134:191-194(1992).
 CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
 CC CAVA.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR INTERPRO; IPR000981; -.
 DR PFAM; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 FT SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 Db 1 C 1

Search completed: February 5, 2001, 12:06:02
 Job time: 279 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:00:49 ; Search time 57.72 Seconds
(without alignments)
8.123 Million cell updates/sec

Title: US-09-687-267-1

Perfect score: 12

Sequence: 1 CXXX 4

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_invertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	6	Q08720	Q08720 homo sapien
2	9	75.0	7	P70804	P70804 azotobacter
3	9	75.0	7	O55184	O55184 rattus norv
4	9	75.0	7	Q66113	Q66113 cherry leaf
5	9	75.0	7	Q67113	Q67113 influenza a
6	9	75.0	7	Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	Q9YIR0	Q9YIR0 human adeno
8	9	75.0	7	Q9YIO9	Q9YIO9 human adeno
9	9	75.0	7	Q42564	Q42564 fugu rubrip
10	9	75.0	8	O32560	O32560 escherichia
11	9	75.0	8	Q15888	Q15888 homo sapien
12	9	75.0	8	Q15890	Q15890 homo sapien
13	9	75.0	8	Q15900	Q15900 homo sapien
14	9	75.0	8	Q9Y4X6	Q9Y4X6 homo sapien
15	9	75.0	8	O02831	O02831 oryctolagus
16	9	75.0	8	Q9TRY3	Q9TRY3 sus sp. ins
17	9	75.0	8	Q9SAY7	Q9SAY7 dioscorea t
18	9	75.0	8	P70243	P70243 mus musculu
19	9	75.0	8	O35835	O35835 rattus norv

20	9	75.0	8	12	Q85562	Q85562 moloney mur
21	9	75.0	8	13	Q90493	Q90493 eopsaltria
22	9	75.0	8	13	Q90498	Q90498 erythrura g
23	9	75.0	8	13	Q91098	Q91098 manorina me
24	9	75.0	9	2	Q47063	Q47063 escherichia
25	9	75.0	9	4	Q15999	Q15999 homo sapien
26	9	75.0	9	4	Q99887	Q99887 homo sapien
27	9	75.0	9	6	Q9XU05	Q9XU05 macropus ru
28	9	75.0	9	6	Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9	Q38340	Q38340 lactococcus
30	9	75.0	9	11	Q9QZ88	Q9QZ88 mus musculu
31	9	75.0	9	11	P97889	P97889 rattus norv
32	9	75.0	9	12	Q69473	Q69473 human herpe
33	9	75.0	9	12	O12096	O12096 caprine art
34	9	75.0	9	12	O12098	O12098 caprine art
35	9	75.0	9	12	O12100	O12100 caprine art
36	9	75.0	9	12	O12102	O12102 caprine art
37	9	75.0	9	12	O12104	O12104 caprine art
38	9	75.0	9	12	O90350	O90350 heparitis g
39	9	75.0	10	2	Q50032	Q50032 mycobacteri
40	9	75.0	10	2	Q47475	Q47475 escherichia
41	9	75.0	10	2	Q48469	Q48469 klebsiella
42	9	75.0	10	2	Q9K343	Q9K343 escherichia
43	9	75.0	10	3	Q9UW2	Q9UW2 schizoplyll
44	9	75.0	10	4	Q13318	Q13318 homo sapien
45	9	75.0	10	4	Q9UN90	Q9UN90 homo sapien

ALIGNMENTS

RESULT 1

ID Q08720 PRELIMINARY; PRT; 6 AA.
AC Q08720;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010691; PubMed=1396344;
RA Waeber G., Habener J.F.;
RT "Novel testis germ cell-specific transcript of the CREB gene contains
RT an alternatively spliced exon with multiple in-frame stop codons.";
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1; -;
FT NON_TER 1
FT NON_TER 6
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

DB 4 C 4

RESULT 2

ID P70804 PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TREMREL. 02, Created)
DT 01-FEB-1997 (TREMREL. 02, Last sequence update)
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)

DE ALGG GENE (FRAGMENT).
GN ALGT.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 1 C 1

RESULT 3
O55184 PRELIMINARY; PRT; 7 AA.
ID O55184;
AC O55184;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
RT expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.
ID Q66113;
AC Q66113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INTA.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain)";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 4 C 4

RESULT 5
Q67113 PRELIMINARY; PRT; 7 AA.
ID Q67113;
AC Q67113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
DB 3 C 3

```
RESULT 6
Q9YVE3
ID Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOMEN;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -.
DR EMBL; AF065065; AAD03662.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 6 C 6

RESULT 7
Q9YI0
ID Q9YI0 PRELIMINARY; PRT; 7 AA.
AC Q9YI0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065067; AAD03666.1; -.
DR EMBL; AF065067; AAD03666.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 6 C 6

RESULT 8
Q9YI09
ID Q9YI09 PRELIMINARY; PRT; 7 AA.
AC Q9YI09;
```

```
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2-G 95-873, RI-67, 55142;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -.
DR EMBL; AF065062; AAD03653.1; -.
DR EMBL; AF065063; AAD03656.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 6 C 6

RESULT 9
O42564
ID O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
DR EMBL; U97673; AAB80916.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 5 C 5

RESULT 10
O32560
ID O32560 PRELIMINARY; PRT; 8 AA.
AC O32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
```

DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DE 01-AUG-1998 (TREMREL. 07, Last annotation update)
 GN PROIONATE KINASE (FRAGMENT).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-W3110;
 RA Hesslinger C., Savers G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ001620; CAA04875.1; -.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 6 C 6

RESULT 11
 Q15888
 ID Q15888 PRELIMINARY; PRT; 8 AA.
 AC Q15888;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-AUG-1998 (TREMREL. 07, Last annotation update)
 DE (CLONE XP15H8A) (FRAGMENT).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32069; AAA73878.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 5 C 5

RESULT 12
 Q15890
 ID Q15890 PRELIMINARY; PRT; 8 AA.
 AC Q15890;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-AUG-1998 (TREMREL. 07, Last annotation update)

DE (CLONE XP19C12A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32083; AAA73880.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 4 C 4

RESULT 13
 Q15900
 ID Q15900 PRELIMINARY; PRT; 8 AA.
 AC Q15900;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-AUG-1998 (TREMREL. 07, Last annotation update)
 DE (CLONE XP7B11A) (FRAGMENT).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32079; AAA73890.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
 DB 2 C 2

RESULT 14
 Q9Y4X6
 ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.
 AC Q9Y4X6;
 DT 01-NOV-1999 (TREMREL. 12, Created)
 DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
 DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
 DE NUCLEAR LIM INTERACTOR (FRAGMENT).
 GN NLI.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

```
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA  Schroth A., Boden J., Royer-Pokora B.;
RT  "Genomic structure, alternative transcripts and chromosomal
RT  localization of the human LIM domain binding protein 1 gene
RT  LDB1/NLI.";
RL  Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
DR  EMBL; AJ243097; CAB45408.1; -.
FT  NON_TER      8
SQ  SEQUENCE      8 AA; 767 MW; EE6EBDD8B862D5B6 CRC64;

Query Match      75.0%; Score 9; DB 4; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 C 1
Db  5 C 5

RESULT 15
O02831
ID  O02831      PRELIMINARY;      PRT;      8 AA.
AC  O02831;
DT  01-JUL-1997 (TrEMBLrel. 04, Created)
DT  01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT  01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE  PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=9637739; PubMed=8783186;
RA  Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
RA  Vuorio E.;
RT  "Evidence for insufficient chondrocytic differentiation during repair
RT  of full-thickness defects of articular cartilage.";
RL  Matrix Biol. 15:39-47(1996).
DR  EMBL; S83371; AAD14433.1; -.
FT  NON_TER      1
SQ  SEQUENCE      8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match      75.0%; Score 9; DB 6; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 C 1
Db  4 C 4
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Search completed: February 5, 2001, 12:05:38
Job time: 289 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:19 ; Search time 42.35 Seconds
(without alignments)
3.230 Million cell updates/sec

Title: US-09-687-267-4

Perfect score: 12

Sequence: 1 KCXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	P10301	Sequence which cor
2	9	75.0	3	P90982	Binding receptor w
3	9	75.0	3	P91660	Synthetic peptide
4	9	75.0	3	R34022	Metal trapping pep
5	9	75.0	3	R34023	Metal trapping pep
6	9	75.0	3	R51439	IGF-1 analogue N-t
7	9	75.0	3	R51440	IGF-1 analogue N-t
8	9	75.0	3	R51441	IGF-1 analogue N-t
9	9	75.0	3	W19847	Human interleukin-
10	9	75.0	3	W56231	Anti-inflammatory
11	9	75.0	3	W56211	Anti-inflammatory
12	9	75.0	3	W56200	Anti-inflammatory

13	9	75.0	3	19	W56172	Anti-inflammatory
14	9	75.0	3	20	W88037	Peptide used in th
15	9	75.0	3	21	Y51896	Biostatin TR232 sy
16	9	75.0	4	2	P10138	Sequence of antiin
17	9	75.0	4	2	P10093	Sequence of peptid
18	9	75.0	4	2	P10382	Enkephalin-like an
19	9	75.0	4	3	P20217	Analgesic and neur
20	9	75.0	4	4	P30083	Sequence of chromo
21	9	75.0	4	4	P30085	Sequence of chromo
22	9	75.0	4	5	P40538	Sequence of cyclic
23	9	75.0	4	5	P40539	Sequence of cyclic
24	9	75.0	4	8	P70833	Sequence encoded b
25	9	75.0	4	10	P91661	Synthetic peptide
26	9	75.0	4	12	R11077	Peptide fragment #
27	9	75.0	4	12	R11079	Peptide fragment #
28	9	75.0	4	12	R11508	Thioredoxin active
29	9	75.0	4	12	R11744	Cyclic platelet ag
30	9	75.0	4	12	R11745	Cyclic platelet ag
31	9	75.0	4	12	R12554	Ocular pressure re
32	9	75.0	4	12	R13935	Antibiotic FK9017
33	9	75.0	4	12	R14723	Farnesyl-protein t
34	9	75.0	4	12	R15751	Farnesyl-protein t
35	9	75.0	4	12	R15752	Farnesyl-protein t
36	9	75.0	4	12	R15753	Farnesyl-protein t
37	9	75.0	4	12	R15754	Farnesyl-protein t
38	9	75.0	4	12	R15755	Farnesyl-protein t
39	9	75.0	4	12	R15756	Farnesyl-protein t
40	9	75.0	4	12	R15757	Farnesyl-protein t
41	9	75.0	4	12	R15758	Farnesyl-protein t
42	9	75.0	4	12	R15759	Farnesyl-protein t
43	9	75.0	4	12	R15760	Farnesyl-protein t
44	9	75.0	4	12	R15761	Farnesyl-protein t
45	9	75.0	4	21	Y80840	Fluorophore-label

ALIGNMENTS

RESULT 1
P10301
ID P10301 standard; Protein; 3 AA.
XX
AC P10301;
XX
DT 19-AUG-1992 (first entry)
XX
DE Sequence which corresp. to residues 19-21 of insulin A chain.
XX
KW Cystine peptide; insulin activity; hormone; diabetes therapy;
KW antidiabetic agent.
XX
OS Mammal.
XX
FH Key
FT Disulfide-bond 2
FT /note= "bonded to Cys(5) of P10115, which is
FT residue 19 of the B chain fragment
FT B15-27"
XX
PN DD147942-A.
XX
PD 29-APR-1981.
XX
PF 01-FEB-1980; 90DD-0011868.
XX
PR 20-AUG-1979; 79DD-0215100.
XX
PA (LOSS/) LOSSE G.
XX
PI Losse G, Stange H;
PI Anti-inflammatory
DR WPI; 1981-53498D/30 (53498D).
XX

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments
XX of insulin A and B chains

XX Claim 1; Page 10; lipp; German.

XX The inventors claim the prepn. of new cysteine peptides with insulin-
CC like activity. The new peptides comprise a sequence with corresp. to
CC a central portion of the insulin B chain (esp. B15-27) and a
CC cysteine-contg. peptide with an AA sequence corresp. to a terminal
CC portion of the insulin A chain (esp. A1-7). The new cysteine
CC peptides are antidiabetic agents with appreciable insulin activity
CC (lower than that of insulin itself) and low antigenic activity.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 2 C 2

RESULT 2

P90982
ID P90982 standard; peptide; 3 AA.

XX AC P90982;

XX DT 06-JUN-1990 (first entry)

XX Binding receptor with selectivity for a target ligand, borne by
DE an article for inactivating toxic materials.

XX Toxic material; inactivator; organophosphorous cpds.; nerve poison;
KW pesticide; decontaminant; military.

XX PN W08902920-A.

XX PD 06-APR-1989.

XX PF 04-OCT-1988; 88WO-US03422.

XX PR 05-OCT-1987; 87US-0105312.

XX PA (LITT) LITTLE AD INC.

XX PI Taylor RF;

XX DR WPI; 1989-114395/15.

XX Article for inactivating toxic materials, eg organo-phosphorous cpds. -
PT comprises solid carrier bearing target ligand binding receptor
PT and ligand-degrading receptor, pref. enzyme

XX Claim 7a; page 42; 57pp; English.

XX The article for inactivating a toxic material comprises a solid carrier
CC bearing a first receptor which binds the target ligand and a second
CC receptor which degrades the target ligand. This synthetic peptide is
CC a preferred first receptor. The article may be used for covering
CC surfaces to protect or decontaminate the surface. The article is esp. for
CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg
CC pesticides and nerve poisons, bacteria and viruses, in environmental,
CC chemical, military and industrial settings.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 2 C 2

RESULT 3

P91660

ID P91660 standard; protein; 3 AA.

XX AC P91660;

XX DT 29-JUN-1990 (first entry)

XX Synthetic peptide corresp. to residues 12-14 of naturally occurring
DE epidermal growth factor (EGF).

XX Epidermal growth factor; angiogenesis; synthetic peptide.

XX Key

FT Misc-difference 1

FT /label=OTHER

FT /note="H-Gly"

FT Misc-difference 3

FT /label=OTHER

FT /note="(aceto amido methyl) NH2-Cys"

XX PN W08901489-A.

XX PD 23-FEB-1989.

XX PF 10-AUG-1988; 88WO-AU00300.

XX PR 10-AUG-1987; 87AU-0003629.

XX PA (CSIR) COMMONWEALTH SCIENT ORG.

XX PI McAuslan BR;

XX DR WPI; 1989-068852/09.

XX Synthetic peptide active in stimulating angiogenesis -
PT has sequences corresponding to amino acid sequences occurring in
PT epidermal growth factor.

XX Claim 3; page 10; lipp; English.

XX The inventors claim synthetic peptides which correspond to sequences
CC occurring in EGF, but excluding EGF. The peptides are angiogenic
CC and have corresp. applications, eg for the healing of wounds and
CC burns. Their relative shortness means that they pose fewer synthesis
CC problems than the entire EGF molecule. They can be admin. singly or
CC association with each other or in association with an angiogenic
CC stimulator.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

DB 3 C 3

RESULT 4

R34022

ID R34022 standard; peptide; 3 AA.

XX AC R34022;

XX 19-MAY-1993 (first entry)
DT Metal trapping peptide intermediate.
XX Electrostatic interaction; metalloprotein; binding site;
DE protecting group.
KW Synthetic.
XX
OS
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 2 /note= "Boc protected"
FT Modified-site 3 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH of cysteine"
FT Modified-site 3 /note= "Ome protected"
FT
PN JP04346999-A.
PD 02-DEC-1992.
XX
XX 24-MAY-1991; 91JJP-0120196.
PF
XX 24-MAY-1991; 91JJP-0120196.
PR (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
PA WPI; 1993-021449/03.
DR
XX New acyclic peptide with metal trapping activity - exhibits in
PT vivo metal transporting action and can be used as drug,
PT diagnostic agent or functional material
XX
PS Claim 3; Page 2; 9pp; Japanese.
XX
CC The acyclic peptide (see R31340) with metal trapping activity may be
CC produced by fragment condensation using the peptide fragments given in
CC R34022-29.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 2 c 2

RESULT 5
R34023
ID R34023 standard; peptide; 3 AA.
XX
AC R34023;
XX
DT 19-MAY-1993 (first entry)
XX
DE Metal trapping peptide intermediate.
XX
KW Electrostatic interaction; metalloprotein; binding site;
KW protecting group.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1 /note= "HCl.H-Val"
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH

FT Modified-site 3 of cysteine"
FT /note= "Ome protected"
XX
PN JP04346999-A.
XX
PD 02-DEC-1992.
XX
PF 24-MAY-1991; 91JJP-0120196.
XX
PR 24-MAY-1991; 91JJP-0120196.
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
PA WPI; 1993-021449/03.
DR
XX New acyclic peptide with metal trapping activity - exhibits in
PT vivo metal transporting action and can be used as drug,
PT diagnostic agent or functional material
XX
PS Claim 3; Page 2; 9pp; Japanese.
XX
CC The acyclic peptide (see R31340) with metal trapping activity may be
CC produced by fragment condensation using the peptide fragments given in
CC R34022-29.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 2 c 2

RESULT 6
R51439
ID R51439 standard; peptide; 3 AA.
XX
AC R51439;
XX
DT 27-OCT-1994 (first entry)
XX
DE IGF-1 analogue N-terminal.
XX
KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
XX
OS Homo sapiens.
XX
PN WO9406445-A.
XX
PD 31-MAR-1994.
XX
PF 02-SEP-1993; 93WO-US08279.
XX
PR 17-SEP-1992; 92US-0947035.
XX (EMBR-) EMBREX INC.
PA (GROP-) GROPEP PTY LTD.
PA (USDA) US SEC OF AGRIC.
XX
XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
PI Walton PE;
XX WPI; 1994-118144/14.
DR
XX Increasing growth of birds - with insulin-like growth factor
PT delivered to the egg before hatching esp. for increasing wt. gain
PT in chickens.
PT

XX Claim 6; Page 37; 45pp; English.
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3
 CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 Db 3 C 3

RESULT 7
 R51440
 ID R51440 standard; peptide; 3 AA.
 XX
 AC R51440;
 XX
 DT 27-OCT-1994 (first entry)
 XX IGF-1 analogue N-terminal.
 DE
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 XX
 XX Homo sapiens.
 OS
 XX WO9406445-A.
 PN
 XX 31-MAR-1994.
 PD
 XX 02-SEP-1993; 93WO-US08279.
 PF
 XX 17-SEP-1992; 92US-0947035.
 PR
 XX (EMBR-) EMBREX INC.
 PA (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 XX WPI; 1994-118144/14.
 DR
 XX Increasing growth of birds - with insulin-like growth factor
 PT delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.
 XX
 XX Claim 6; Page 37; 45pp; English.
 PS Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 Db 3 C 3

RESULT 8
 R51441
 ID R51441 standard; peptide; 3 AA.
 XX
 AC R51441;
 XX
 DT 27-OCT-1994 (first entry)
 XX IGF-1 analogue N-terminal.
 DE
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 XX
 XX Homo sapiens.
 OS
 XX WO9406445-A.
 PN
 XX 31-MAR-1994.
 PD
 XX 02-SEP-1993; 93WO-US08279.
 PF
 XX 17-SEP-1992; 92US-0947035.
 PR
 XX (EMBR-) EMBREX INC.
 PA (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 XX WPI; 1994-118144/14.
 DR
 XX Increasing growth of birds - with insulin-like growth factor
 PT delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.
 XX
 XX Claim 6; Page 37; 45pp; English.
 PS Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3
 CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 C 2
 Db 3 C 3

RESULT 9
 W19847
 ID W19847 standard; Peptide; 3 AA.
 AC W19847;
 XX
 XX 23-SEP-1997 (first entry)
 DT
 DE Human interleukin-12 p40 subunit N-terminal peptide.
 XX
 XX Interleukin-12; Fc gamma-1; immunosuppressive; autoimmune disease;
 KW graft rejection; toxic shock; therapy.
 RW
 XX Homo sapiens.
 OS
 XX WO9720062-A1.
 FN
 XX 05-JUN-1997.
 PD
 XX 02-DEC-1996; 96WO-US19181.
 PF
 XX 01-DEC-1995; 95US-0565856.
 PR
 XX (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 PA (UTMA-) UNIV MASSACHUSETTS.
 PA
 XX Steel AW, Strom TB;
 XX WPI; 1997-310615/28.
 DR N-PSDB; T72095-96.
 XX
 XX Fusion protein containing interleukin-12 p40 sub-unit - has
 PT increased stability, used to inhibit graft rejection, or treat
 PT autoimmune disease and endotoxin-induced shock
 XX
 XX Example; Fig 2; 36pp; English.

CC A peptide (W19847) comprises the three N-terminal amino acid
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is
 CC encoded both by native human p40 cDNA (T72096) and by a primer
 CC (T72095) based on the native sequence. PCR amplification has
 CC been used to amplify p40 cDNA. A fusion protein comprising the
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed
 CC in E. coli. This fusion protein has a longer in vivo half-life
 CC than native p40 and can be used as an immunosuppressive (e.g. to
 CC treat autoimmune diseases or to inhibit graft rejection) or to
 CC treat or prevent endotoxin-induced shock.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 C 2
 Db 2 C 2

RESULT 10
 W56231
 ID W56231 standard; peptide; 3 AA.
 XX
 AC W56231;
 XX
 XX 20-JUL-1998 (first entry)
 DT
 DE Anti-inflammatory tripeptide.
 DE
 XX Anti-inflammatory; macrophage inhibitory activity; fibronectin;
 KW T-cell inhibitory activity; adherence; extracellular matrix;
 KW up-regulation; fas receptor expression; inflammation.
 XX
 OS Synthetic.
 XX
 XX WO9809985-A2.
 FN
 XX 12-MAR-1998.
 PD
 XX 03-SEP-1997; 97WO-IL00295.
 PF
 XX 28-MAY-1997; 97US-0864301.
 PR 03-SEP-1996; 96US-0025376.
 PR 20-NOV-1996; 96US-0753141.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX Beserman P, Eisenbachschwartz M, Hirschberg DL;
 PI WPI; 1998-193550/17.
 DR
 XX Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease
 XX
 XX Claim 7; Page 35; 42pp; English.

CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
 CC Xaa = any amino acid residue.
 CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.

SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 C 2
 Db 3 C 3

OS Synthetic.
XX WO9809985-A2.
XX
XX PD 12-MAR-1998.
XX
XX PF 03-SEP-1997; 97WO-IL00295.
XX
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX DR WPI; 1998-193550/17.
XX
XX PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
XX PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
XX PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX
XX PS Claim 3; Page 34; 42pp; English.
XX
XX CC W56171-248 represent anti-inflammatory tripeptides of the invention.
XX CC They are derived from the formulae:
XX CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
XX CC Xaa = any amino acid residue.
XX CC Cyclic derivatives of the peptides also function as anti-inflammatory
XX CC agents. The peptides can be covalently linked to one another either
XX CC directly or through a spacer. The peptides and their derivatives have
XX CC macrophage inhibitory and T-cell inhibitory activity and thus,
XX CC anti-inflammatory activity. The peptides and compositions have
XX CC anti-immune activity, i.e. inhibitory effects against a cellular and
XX CC humoral immune response, including a response not associated with
XX CC inflammation. The peptides also inhibit the ability of macrophages and
XX CC T-cells to adhere to extracellular matrix components and fibronectin, as
XX CC well as up-regulated fas receptor expression in T-cells. They can be used
XX CC to inhibit unwanted immune reaction and inflammation.
XX
XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
I
Db 1 C 1

RESULT 14
W88037
ID W88037 standard; peptide; 3 AA.
XX
XX AC W88037;
XX
XX DT 09-APR-1999 (first entry)
XX
XX DE Peptide used in the hair composition of the invention.
XX
XX KW Hair; styling; wave.
XX
XX OS Synthetic.
XX
XX PN JP11012138-A.
XX
XX PD 19-JAN-1999.
XX
XX PF 18-JUN-1997; 97JP-0161657.
XX

PR 18-JUN-1997; 97JP-0161657.
XX
XX PA (LIOY) LION CORP.
XX
XX DR WPI; 1999-148442/13.
XX
XX PT New composition for hair - comprises oligopeptide having more than 2
XX PT cysteine residues and reducing agent
XX
XX PS Example 2; Page 6; 17pp; Japanese.
XX
XX CC Peptides W88033-39 are used in the hair composition of the invention.
XX CC The specification describes a hair composition that comprises at
XX CC least one oligopeptide having more than two cysteine residues and more
XX CC than three amino acid residues of the same kind (except cysteine) and a
XX CC reducing agent. The composition is useful for styling hair to take
XX CC various shapes and waves safely and effectively.
XX
XX SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 20; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
I
Db 1 C 1

RESULT 15
Y51896
ID Y51896 standard; peptide; 3 AA.
XX
XX AC Y51896;
XX
XX DT 16-JUN-2000 (first entry)
XX
XX DE Biostatin TT232 synthesising peptide 1.
XX
XX KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;
XX KW cellular proliferation inhibition; somatostatin; antitumor.
XX
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "TFA*Lys(2)"
XX FT Modified-site 2 /note= "Cys(Acm)"
XX FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"
XX
XX PN WO200011032-A2.
XX
XX PD 02-MAR-2000.
XX
XX PF 20-AUG-1999; 99WO-EP06131.
XX
XX PR 20-AUG-1998; 98WO-EP05306.
XX
XX PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.
XX
XX PI Braum G, Liffeith A, Birr C;
XX
XX DR WPI; 2000-224663/19.
XX
XX PT Biostatin preparation in high yield by solid synthesis, including
XX PT closure of disulfide bridge before cleavage from support, useful as
XX PT antitumor agent
XX
XX PS Example 4; Page 23; 33pp; German.
XX

CC This invention describes a novel method for the solid phase (SP)
CC synthesis of biostatin (TT 232) (I) which includes closing the disulfide
CC bridge by oxidation of the completely or partially constructed peptide
CC while still bonded to the solid phase. The products of the invention have
CC cytotostatic activity and are tyrosine kinase inhibitors. (I) inhibits the
CC tyrosine kinase activity of various human stomach cancer cell lines and
CC thus inhibits cellular proliferation. The heptapeptide (I) described in
CC the invention is a somatostatin analog which shows strong antitumor
CC activity in vitro and in vivo. The SP synthesis method gives (I) is more
CC easily and in markedly higher yield than by the method of EP505680, in
CC which the cyclization is carried out after cleaving the peptide from the
CC resin. The solution method is also a simple synthesis of (I) in high
CC yield; typically the tert-butyl-protected precursor can be oxidized in
CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the
CC synthesis of biostatin TT232 described in the method of the invention.

XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 2 C 2

Search completed: February 5, 2001, 12:01:19
Job time: 366 sec

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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:53 ; Search time 30.91 Seconds
(without alignments)
2.324 Million cell updates/sec

Title: US-09-687-267-4
Perfect score: 12
Sequence: 1 XCXX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*

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2: /cgn2.6/ptodata/2/1aa/5B_COMB.pep.*

3: /cgn2.6/ptodata/2/1aa/6_COMB.pep.*

4: /cgn2.6/ptodata/2/1aa/PCTUS_COMB.pep.*

5: /cgn2.6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-386-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-399-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	2	3	US-07-791-213D-22
22	9	75.0	2	3	US-07-791-213D-38
23	9	75.0	2	3	US-07-945-982-2
24	9	75.0	2	3	US-07-945-982-8
25	9	75.0	2	3	US-07-947-035-3
26	9	75.0	2	3	US-07-947-035-4
27	9	75.0	2	3	US-07-947-035-5
28	9	75.0	2	3	US-08-285-443-4

29	9	75.0	3	1	US-08-079-812-31	Sequence 31, Appl
30	9	75.0	3	1	US-08-122-510-11	Sequence 11, Appl
31	9	75.0	3	1	US-08-122-510-12	Sequence 12, Appl
32	9	75.0	3	1	US-08-122-510-13	Sequence 13, Appl
33	9	75.0	3	1	US-07-789-913-26	Sequence 26, Appl
34	9	75.0	3	1	US-08-371-930-4	Sequence 4, Appl
35	9	75.0	3	1	US-08-049-794-26	Sequence 26, Appl
36	9	75.0	3	1	US-08-372-455-2	Sequence 2, Appl
37	9	75.0	3	1	US-08-372-455-8	Sequence 8, Appl
38	9	75.0	3	1	US-08-321-585A-1	Sequence 1, Appl
39	9	75.0	3	1	US-08-321-585A-2	Sequence 2, Appl
40	9	75.0	3	1	US-08-321-585A-3	Sequence 3, Appl
41	9	75.0	3	1	US-08-446-908-14	Sequence 14, Appl
42	9	75.0	3	1	US-08-293-150A-22	Sequence 22, Appl
43	9	75.0	3	1	US-08-293-150A-38	Sequence 38, Appl
44	9	75.0	3	1	US-08-447-515-12	Sequence 12, Appl
45	9	75.0	3	3		

ALIGNMENTS

RESULT 1

US-07-791-213D-23

; Sequence 23, Application US/07791213D

; Patent No. 5409895

; GENERAL INFORMATION:

; APPLICANT: MORISHITA, Hideaki

; APPLICANT: KANAMORI, Toshinori

; APPLICANT: NOBUHARA, Masahiro

; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE

; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME

; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

; TITLE OF INVENTION: TREATING USING THE SAME

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/791,213D

; FILING DATE: 13-NOV-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-306745

; FILING DATE: 13-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 029650-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 2 C 2

RESULT 2
US-07-791-213D-39
; Sequence 39, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-39

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 3
US-08-133-804-9
; Sequence 9, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,804
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-133-804-9

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 2 C 2

RESULT 4
US-08-354-240A-12
; Sequence 12, Application US/08354240A
; Patent No. 5670356;
; GENERAL INFORMATION:
; APPLICANT: Sherf, Bruce A.
; APPLICANT: Wood, Keith V.
; TITLE OF INVENTION: MODIFIED LUCIFERASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1514
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,240A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506.029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

RESULT 5
US-08-461-838-9
Sequence 9, Application US/08461838
Patent No. 5753204
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..2
OTHER INFORMATION: /note= "C-Terminal tail (Ser-Cys)"
US-08-461-838-9

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

RESULT 6
US-08-293-150A-23
Sequence 23, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 2 C 2

RESULT 7
US-08-293-150A-39
Sequence 39, Application US/08293150A

Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293.150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2
Db 1 C 1

RESULT 8
US-08-461-386-9
Sequence 9, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1-2
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 C 2
Db 2 C 2

RESULT 9
US-08-465-380-307
Sequence 307, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gausemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.380
FILING DATE: June 5, 1995
CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/268
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 10
US-08-486-397-307
;; Sequence 307, Application US/08486397
;; Patent No. 5866542
;; GENERAL INFORMATION:
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
;; APPLICANT: Peter W. Bergum
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
;; NUMBER OF SEQUENCES: 357
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,397
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/269
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 11
US-08-486-399-307
;; Sequence 307, Application US/08486399
;; Patent No. 5866543
;; GENERAL INFORMATION:
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
;; APPLICANT: Peter W. Bergum
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
;; NUMBER OF SEQUENCES: 356
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,399
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/270
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 12

US-08-461-965-307
; Sequence 307, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 13

US-08-634-641-307
; Sequence 307, Application US/08634641
; Patent No. 5955294
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George P. Vlasuk
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Menssens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Josef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,641
; FILING DATE: April 19, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 14

US-08-818-253-52
; Sequence 52, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALITES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997

PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 15

US-09-249-471-307
; Sequence 307, Application US/09249471
; Patent No. 6040441
; GENERAL INFORMATION:

APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berqum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,471
; FILING DATE:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

APPLICATION NUMBER: 08/465,380

APPLICATION NUMBER: 08/461,965

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 307:

SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid

TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment

FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an

OTHER INFORMATION: amino acid.
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

Search completed: February 5, 2001, 12:01:53
Job time: 335 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:02:32 ; Search time 34.92 Seconds
(without alignments)
7.778 Million cell updates/sec

Title: US-09-687-267-4

Perfect score: 12

Sequence: 1 XCXX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	3	2 A22565	R-phycoerythrin al
2	9	75.0	4	2 I51049	metallothionein-A
3	9	75.0	4	2 S43959	Ig mu chain V regi
4	9	75.0	4	2 S52238	pallidipin - assas
5	9	75.0	5	2 A22565	R-phycoerythrin al
6	9	75.0	5	2 F22565	R-phycoerythrin ga
7	9	75.0	5	2 A33882	cadmium-binding pe
8	9	75.0	5	2 B45525	actin I - malaria
9	9	75.0	5	2 S57266	hemoglobin, extrac
10	9	75.0	6	2 J00355	lipopeptide W51279
11	9	75.0	6	2 C22565	R-phycoerythrin be
12	9	75.0	6	2 I37027	protamine P1 - gor
13	9	75.0	6	2 I37263	Y protein - human
14	9	75.0	6	2 S29881	Na+/K+-exchanging
15	9	75.0	6	2 H48394	glycoprotein compo
16	9	75.0	6	2 I67345	MHC H2-K-k cell su
17	9	75.0	6	2 I65546	MHC H2-L antigen -
18	9	75.0	6	2 P10652	T-cell receptor be.
19	9	75.0	6	2 F41946	laminin B1 - weste
20	9	75.0	6	2 I49421	hypothetical TCl3
21	9	75.0	6	2 I79564	Ig heavy chain V r
22	9	75.0	7	2 PH1408	venom heptapeptide
23	9	75.0	7	2 A58512	hypothetical prote
24	9	75.0	7	2 S08606	mabinlin II chain
25	9	75.0	7	2 S38516	cadmium-binding he
26	9	75.0	7	2 B34818	acetylcholinestera
27	9	75.0	7	2 B33882	formylglycinamide
28	9	75.0	7	2 A34026	
29	9	75.0	7	2 A12016	

30 9 75.0 7 2 PH1602 Ig H chain V-D-J r
31 9 75.0 7 2 PH0932 T-cell receptor be
32 7 4 I56695 hypothetical I2 pr
33 9 75.0 8 2 PH1407 Ig heavy chain V r
34 9 75.0 8 2 S59622 metallothionein is
35 9 75.0 8 2 XGHUEU urine glycopeptide
36 9 75.0 8 2 A25836 L-serine dehydrata
37 9 75.0 8 2 PC1002 leucine--trNA liga
38 9 75.0 8 2 S19288 acylase - Kluyvera
39 9 75.0 8 2 A37521 R-phycoerythrin ga
40 9 75.0 8 2 C61512 variant surface gl
41 9 75.0 8 2 D61512 variant surface gl
42 9 75.0 8 2 PH1618 Ig H chain V-D-J r
43 9 75.0 8 2 PH0803 T-cell receptor al
44 9 75.0 8 2 I57018 gene Cfr protein
45 9 75.0 8 2 PH0934 T-cell receptor be

ALIGNMENTS

RESULT 1

A22565

R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: A22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: A22565

A:Molecule type: protein

A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; MUID:95324545

A:Accession: I51049

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 4 C 4

RESULT 3

S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 2 C 2

RESULT 4

S55238

pallidipin - assassin bug (fragment)

C:Species: Triatoma pallidipennis (assassin bug)

C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000

C:Accession: S55238

R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuning

Biochem. J. 307, 465-470, 1995

A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib

A:Reference number: S55238; MUID:95251610

A:Accession: S55238

A:Molecule type: protein

A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 3 C 3

RESULT 5

B22565

R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: B22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: B22565

A:Molecule type: protein

A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 2 C 2

RESULT 6

F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: F22565

A:Molecule type: protein

A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 3 C 3

RESULT 7

A33882

cadmium-binding pentapeptide - downy thornapple

C:Species: Datura innoxia (downy thornapple)

C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993

C:Accession: A33882

R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.

Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987

A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plan

A:Reference number: A94182; MUID:88016144

A:Accession: A33882

A:Molecule type: protein

A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 2 C 2

RESULT 8

B45525

actin I - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum

C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000

C:Accession: B45525

R:Wesseling, J.G.; Shijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoc:

Mol. Biochem. Parasitol. 35, 167-176, 1989

A:Title: Stage-specific expression and genomic organization of the actin genes of the

A:Reference number: A45525; MUID:89364996

A:Accession: B45525

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <WES>

A:Cross-references: GB:J03988

A>Note: the authors translated the codon GAA for residue 3 as Gly

C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 4 C 4

RESULT 9
S65726
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65726
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A>Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A:Reference number: S65721; MUID:96176855
A:Accession: S65726
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 4 C 4

RESULT 10
JU0355
lipopeptide WSL279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JU0355
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A>Title: Structure and synthesis of an immunoreactive lipopeptide, WSL279, of microbial origin
A:Reference number: JU0355; MUID:91300586
A:Accession: JU0355
A:Molecule type: protein
A:Residues: 1-6 <TSU>
A>Note: the structure was confirmed by synthesis
C:Keywords: blocked amino end; lipoprotein
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 11
C22565
R-phycocerythrin beta-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A>Title: Characterization of the bilin attachment sites in R-phycocerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 4 C 4

RESULT 12
I37027
protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A>Title: Identification of conserved potential regulatory sequences of the protamine-c-
A:Reference number: I37013; MUID:94040810
A:Accession: I37027
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 6 C 6

RESULT 13
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waechter, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A>Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative
A:Reference number: I37263; MUID:93010691
A:Accession: I37263
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 4 C 4

RESULT 14
S29881
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S29881
R:Waelderhaug, M.O.; Post, R.L.; Saccamani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A>Title: Structural relatedness of three ion-transport adenosine triphosphatases arou
A:Reference number: S29881; MUID:85131201
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney

C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F:4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
I
DB 2 C 2

RESULT 15

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: H48394
R:Mathier, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A:Reference number: A48394; MUID:93250576
A:Accession: H48394
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <MAT>
A:Experimental source: milk
A:Note: sequence extracted from NCBI backbone (NCBIP:131518)
C:Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
I
DB 6 C 6

Search completed: February 5, 2001, 12:02:32
Job time: 289 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:06:02 ; Search time 20.72 Seconds

(without alignments)
6.234 Million cell updates/sec

Title: US-09-687-267-4

Perfect score: 12

Sequence: 1 XCXX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB ID	Description
1	9	75.0	8 1 ACT_CARMA	P80709 carcinus ma
2	9	75.0	8 1 GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9 1 CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9 1 CONO_CONGE	P05486 conus geogr
5	9	75.0	9 1 CONO_CONST	P05487 conus stria
6	9	75.0	9 1 DNF1_LOCHI	P16339 locusta mig
7	9	75.0	9 1 ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9 1 MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9 1 OXYA_SCYCA	P42996 scyllorhinu
10	9	75.0	9 1 OXYA_SQUAC	P42997 scyllorhinu
11	9	75.0	9 1 OXYF_SCYCA	P42995 bufo regula
12	9	75.0	9 1 OXYT_BUFRE	P23879 cyprinus ca
13	9	75.0	9 1 OXYT_CYPCA	P42998 eisenia foe
14	9	75.0	9 1 OXYT_EISFO	P80027 octopus vul
15	9	75.0	9 1 OXYT_OCTVU	P32878 ocyrtolagus
16	9	75.0	9 1 OXYT_RABIT	P42994 raja clavat
17	9	75.0	9 1 OXYT_RAJCL	P43000 squalus aca
18	9	75.0	9 1 OXYT_SQUAC	OS4296 salmoneilla
19	9	75.0	9 1 RS11_SALTY	P24047 stomopneute
20	9	75.0	9 1 SAP_STOVA	P17440 pichia jadi
21	9	75.0	9 1 TAL1_PICJA	P17441 pichia jadi
22	9	75.0	9 1 TAL3_PICJA	P02728 homo sapien
23	9	75.0	10 1 GLEM_HUMAN	P80678 cheilosoma
24	9	75.0	10 1 GON2_CHEPR	P81084 pinus pinas
25	9	75.0	10 1 RCA_PINPS	P50983 conus imper
26	9	75.0	12 1 CXA1_CONIM	O22426 lotus japon
27	9	75.0	12 1 NO40_LOTJA	O24369 sesbania ro
28	9	75.0	12 1 NO40_SESRO	P55960 glycine max
29	9	75.0	12 1 NO40_SOYBN	P36207 ginkgo bilo
30	9	75.0	12 1 RR16_GINBI	P01371 tremella me
31	9	75.0	12 1 TAL0_TREME	P04558 catostomus
32	9	75.0	12 1 UR2A_CATCO	P04559 catostomus
33	9	75.0	12 1 UR2B_CATCO	

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34 9 75.0 12 1 UR2B_CYPCA
35 9 75.0 12 1 UR2_GILMI
36 9 75.0 12 1 UR2_POLSP
37 9 75.0 12 1 UR2_SCYCA
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39 9 75.0 13 1 ACT7_SOYBN
40 9 75.0 13 1 CXA1_CONST
41 9 75.0 13 1 CXA2_CONGE
42 9 75.0 13 1 CXAA_CONST
43 9 75.0 13 1 CXET_CONTE
44 9 75.0 13 1 GER1_HORVU
45 9 75.0 13 1 GER2_HORVU

P04561 cyprinus ca
P01147 grillichthys
P81022 polyodon sp
P35490 scyllorhinu
P17776 escherichia
P15987 glycine max
P15471 conus stria
P01520 conus geogr
P28878 conus stria
P81755 conus texti
P28525 hordeum vul
P28526 hordeum vul

ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN (FRAGMENT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 KDA.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC INTERPRO: IPR000279;
DR PROSITE: PS00405; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;
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ALIGNMENTS

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RESULT 1
ACT_CARMA STANDARD; PRT; 8 AA.
ID ACT_CARMA
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN (FRAGMENT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.;
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 KDA.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC INTERPRO: IPR000279;
DR PROSITE: PS00405; ACTINS_1; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 2 C 2

RESULT 2
GLUR_HUMAN STANDARD; PRT; 8 AA.
ID GLUR_HUMAN
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
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RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA • Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem. J. 123:25p-25P(1971).
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR: A03188; XGHUEU.
KW Glycoprotein.
FT CARBOHYD 1 1 S-LINKED (GAL. .).
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 3
CCAP_CARMA STANDARD; PRT; 9 AA.
ID C38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CARDIOACTIVE PEPTIDE (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C. MAENAS; TISSUE=PERICARDIAL ORGANS;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M. SEXTA;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T. MOLITOR, AND S. ERIDANIA; TISSUE=HEAD;
RX MEDLINE=94176032; PubMed=8129851;
RA Furiya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYMPH.
DR PIR: A26363; A26363.
DR PIR: A27233; S27233.
KW Neuropeptide; Amidation.
FT MOD_RES 3 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 3 C 3

RESULT 4
CONO_CONGE STANDARD; PRT; 9 AA.
ID P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LYS-CONOPRESSIN G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: A28495; A28495.
DR INTERPRO: IPR000981;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
|
Db 1 C 1

RESULT 5
CONO_CONST STANDARD; PRT; 9 AA.
ID P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ARG-CONOPRESSIN S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]

RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: B28495; B28495.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 DB 1 C 1

RESULT 6
 DNFL_LOCMI STANDARD; PRT; 9 AA.
 AC P16339;
 DT 01-AUG-1990 (Rel. 15; Created)
 DT 01-AUG-1990 (Rel. 15; Last sequence update)
 DT 15-DEC-1998 (Rel. 37; Last annotation update)
 DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 RN [1]

RP SEQUENCE.
 RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;
 RX MEDLINE=88077077; PubMed=3689410;
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
 RA Delaage M., Schooley D.A.;
 RT "Identification of an arginine vasopressin-like diuretic hormone from
 RT Locusta migratoria.";
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
 CC -!- FUNCTION: DIURETIC HORMONE.
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: A29477; A29477.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT DISULFID 1 6 IN F1.
 FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
 FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 DB 1 C 1

RESULT 7
 ISOT_CYPCA
 ID ISOT_CYPCA STANDARD; PRT; 9 AA.

AC P42993;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 01-NOV-1995 (Rel. 32; Last annotation update)
 DE ISOTOCIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 RN [1]

RP SEQUENCE.
 RC TISSUE=PIUITARY;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony
 RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
 RT water bony fish.";
 RL Comp. Biochem. Physiol. 14:245-254(1965).
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: A61364; A61364.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 DB 1 C 1

RESULT 8
 MGMT_BOVIN
 ID MGMT_BOVIN STANDARD; PRT; 9 AA.

AC P29177;
 DT 01-DEC-1992 (Rel. 24; Created)
 DT 01-DEC-1992 (Rel. 24; Last sequence update)
 DT 01-OCT-1996 (Rel. 34; Last annotation update)
 DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).
 GN MGMT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]

RP SEQUENCE.
 RC TISSUE=THYMUS;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B., Hall J., Karan P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 RT methyltransferase.";
 RL Nucleic Acids Res. 18:17-21(1990).
 CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
 CC IRREVERSIBLY INACTIVATED.
 CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN
 CC L-CYSTEINE -> DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-
 CC L-CYSTEINE.
 CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
 DR INTERPRO: IPR001497; -.

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DR PROSITE: PS00374; MGMT: PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 9 C 9

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PIUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: aspartocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
DR Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

RESULT 10
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN (ASPARTOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;

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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CC INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
DR Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PIUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: aspartocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CC INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
DR Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
DB 1 C 1

RESULT 12
OXYT_BUFRE

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ID OXYT_BUFE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE SERITOCIN.
OS Bufo regularis (African toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY NEUROINTERMEDIATE LOBE;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 13
OXYT_CYPCA
ID OXYT_CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE VASOTOCIN.
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C. CARPIO; TISSUE=PITUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fish.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. MARINUS; TISSUE=PITUITARY;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: B61364; B61364.
DR PIR: S06375; S06375.
DR INTERPRO: IPR000981; -;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 14
OXYT_EISFO STANDARD; PRT; 9 AA.
ID OXYT_EISFO STANDARD; PRT; 9 AA.
AC P42998;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ANNETOCIN.
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eisenia.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=94121660; PubMed=8292046;
RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
RT Eisenia foetida.";
RL Biochem. Biophys. Res. Commun. 198:393-398(1994).
CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
CC NEPHRIDIAL FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: PC2021; PC2021.
DR INTERPRO: IPR000981; -;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; D4EE76EB45412C9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 15
OXYT_OCTVU STANDARD; PRT; 9 AA.
ID OXYT_OCTVU STANDARD; PRT; 9 AA.
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CEPHALOTOCIN.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
RN [1]
RP SEQUENCE.
RC TISSUE=NERVE ENDINGS;

RX MEDLINE-92270139; PubMed-1589145;
RA Reich G.;
RT "A new peptide of the oxytocin/vasopressin family isolated from
RT nerves of the cephalopod Octopus vulgaris.";
RL Neurosci. Lett. 134:191-194(1992).
CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
CC CAVA.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

Search completed: February 5, 2001, 12:06:02
Job time: 279 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:05:38 ; Search time 57.72 Seconds
(without alignments)
8.123 Million cell updates/sec

Title: US-09-687-267-4
Perfect score: 12
Sequence: 1 XCXX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	6	4 Q08720	Q08720 homo sapien
2	9	75.0	7	2 P70804	P70804 azotobacter
3	9	75.0	7	11 O55184	O55184 rattus norv
4	9	75.0	7	12 Q66113	Q66113 cherry leaf
5	9	75.0	7	12 Q67113	Q67113 influenza a
6	9	75.0	7	12 Q9YVE3	Q9YVE3 human adeno
7	9	75.0	7	12 Q9YI90	Q9YI90 human adeno
8	9	75.0	7	12 Q9YI09	Q9YI09 human adeno
9	9	75.0	7	13 Q42564	Q42564 figu rubrip
10	9	75.0	8	2 O32560	O32560 escherichia
11	9	75.0	8	4 Q15888	Q15888 homo sapien
12	9	75.0	8	4 Q15890	Q15890 homo sapien
13	9	75.0	8	4 Q15900	Q15900 homo sapien
14	9	75.0	8	4 Q9Y4X6	Q9Y4X6 homo sapien
15	9	75.0	8	6 O02831	O02831 oryctolagus
16	9	75.0	8	6 Q9TRY3	Q9TRY3 sus sp. ins
17	9	75.0	8	10 Q9SAY7	Q9SAY7 dioscorea t
18	9	75.0	8	11 P70243	P70243 mus musculu
19	9	75.0	8	11 O35835	O35835 rattus norv

20	9	75.0	8	12 Q85562	Q85562 moloney mur
21	9	75.0	8	13 Q90493	Q90493 eopsaltria
22	9	75.0	8	13 Q90498	Q90498 erythrura g
23	9	75.0	8	13 Q91098	Q91098 manorina me
24	9	75.0	9	2 Q47063	Q47063 escherichia
25	9	75.0	9	4 Q15999	Q15999 homo sapien
26	9	75.0	9	4 Q99887	Q99887 homo sapien
27	9	75.0	9	6 Q9XT05	Q9XT05 macropus ru
28	9	75.0	9	6 Q9TUY0	Q9TUY0 monodelphis
29	9	75.0	9	9 Q38340	Q38340 lactococcus
30	9	75.0	9	11 Q9QZ88	Q9QZ88 mus musculu
31	9	75.0	9	11 P97889	P97889 rattus norv
32	9	75.0	9	12 Q69473	Q69473 human herpe
33	9	75.0	9	12 O12096	O12096 caprine art
34	9	75.0	9	12 O12098	O12098 caprine art
35	9	75.0	9	12 O12100	O12100 caprine art
36	9	75.0	9	12 O12102	O12102 caprine art
37	9	75.0	9	12 O12104	O12104 caprine art
38	9	75.0	9	12 Q90350	Q90350 hepatitis g
39	9	75.0	10	2 Q50032	Q50032 mycobacteri
40	9	75.0	10	2 Q47475	Q47475 escherichia
41	9	75.0	10	2 Q48469	Q48469 klebsiella
42	9	75.0	10	2 Q9K343	Q9K343 escherichia
43	9	75.0	10	3 Q9UYW2	Q9UYW2 schizophyll
44	9	75.0	10	4 Q13318	Q13318 homo sapien
45	9	75.0	10	4 Q9UN90	Q9UN90 homo sapien

ALIGNMENTS

RESULT 1

Q08720 PRELIMINARY; PRT; 6 AA.
AC Q08720; DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010691; PubMed=1396344;
RA Waeber G., Habener J.F.;
RT "Novel testis germ cell-specific transcript of the CREB gene contains
RT an alternatively spliced exon with multiple in-frame stop codons."
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1; -.
FT NON_TER 1
FT NON_TER 6
SQ SEQUENCE 6 AA: 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2

Db 4 C 4

RESULT 2

P70804 PRELIMINARY; PRT; 7 AA.
ID P70804; AC P70804;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)

DE ALG GENE (FRAGMENT).
GN ALGT.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 1 C 1

RESULT 3
O55184 PRELIMINARY; PRT; 7 AA.
AC O55184;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
RT expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 3 C 3

RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.
ID Q66113;
AC Q66113;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).
OS cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain).";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
KW Repeat.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 4 C 4

RESULT 5
Q67113 PRELIMINARY; PRT; 7 AA.
ID Q67113;
AC Q67113;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
KW Hemagglutinin.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 3 C 3

```
RESULT 6
Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOMEN;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -.
DR EMBL; AF065065; AAD03662.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 6 C 6

RESULT 7
Q9YI90 PRELIMINARY; PRT; 7 AA.
AC Q9YI90;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -.
DR EMBL; AF065066; AAD03664.1; -.
DR EMBL; AF065067; AAD03666.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 6 C 6

RESULT 8
Q9YIQ9 PRELIMINARY; PRT; 7 AA.
AC Q9YIQ9;
```

```
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z-G 95-873, RI-67, 55142;
RA Crawford-Miksz L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing
RT acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -.
DR EMBL; AF065062; AAD03653.1; -.
DR EMBL; AF065063; AAD03656.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 6 C 6

RESULT 9
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564;
AC O42564;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
FT IONIC CHANNEL.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
Db 5 C 5

RESULT 10
O32560 PRELIMINARY; PRT; 8 AA.
ID O32560;
AC O32560;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
```

DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)
 DE PROPIONATE KINASE (FRAGMENT).
 GN TDCD.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W3110;
 RA Hesslinger C., Savers G.;
 RL Submitted (SEP-1997) to the EMBL/genbank/DBJ databases.
 RL Submitted (SEP-1997) to the EMBL/genbank/DBJ databases.
 DR EMBL; AJ001620; CAA04875.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 Db 6 C 6

RESULT 11
 Q15888
 ID Q15888 PRELIMINARY; PRT; 8 AA.
 AC Q15888;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)
 DE (CLONE XP15H8A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32069; AAA73878.1; -.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 Db 5 C 5

RESULT 12
 Q15890
 ID Q15890 PRELIMINARY; PRT; 8 AA.
 AC Q15890;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)

DE (CLONE XP19G12A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32083; AAA73880.1; -.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 Db 4 C 4

RESULT 13
 Q15900
 ID Q15900 PRELIMINARY; PRT; 8 AA.
 AC Q15900;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-AUG-1998 (TREMELrel. 07, Last annotation update)
 DE (CLONE XP7B11A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32079; AAA73890.1; -.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 Db 2 C 2

RESULT 14
 Q9Y4X6
 ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.
 AC Q9Y4X6;
 DT 01-NOV-1999 (TREMELrel. 12, Created)
 DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
 DE NUCLEAR LIM INTERACTOR (FRAGMENT).
 GN NLI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
 RA Schroth A., Bodem J., Royer-Pokora B.;
 RT "Genomic structure, alternative transcripts and chromosomal
 RT localization of the human LIM domain binding protein 1 gene
 RT LDB1/NLI.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ243097; CAB45408.1; -;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 767 MW; EE6EBDEB862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 |
 Db 5 C 5

RESULT 15
 002831
 ID O02831 PRELIMINARY; PRT; 8 AA.
 AC O02831;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96377339; PubMed=8783186;
 RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
 RA Vuorio E.;
 RT "Evidence for insufficient chondrocytic differentiation during repair
 RT of full-thickness defects of articular cartilage.";
 RL Matrix Biol. 15:39-47(1996).
 DR EMBL; S83371; AAD14433.1; -;
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 C 2
 |
 Db 4 C 4

Search completed: February 5, 2001, 12:05:38
 Job time: 289 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:19 ; Search time 42.35 Seconds
(without alignments)
3.230 Million cell updates/sec

Title: US-09-687-267-5

Perfect score: 12
Sequence: 1 XXCX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_36.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	P10301	Sequence which cor
2	9	75.0	3	P90382	Binding receptor w
3	9	75.0	3	P91660	Synthetic peptide
4	9	75.0	3	R34022	Metal trapping pep
5	9	75.0	3	R34023	Metal trapping pep
6	9	75.0	3	R51439	IGF-1 analogue N-t
7	9	75.0	3	R51440	IGF-1 analogue N-t
8	9	75.0	3	R51441	IGF-1 analogue N-t
9	9	75.0	3	W19847	Human interleukin-
10	9	75.0	3	W56231	Anti-inflammatory
11	9	75.0	3	W56211	Anti-inflammatory
12	9	75.0	3	W56200	Anti-inflammatory

13	9	75.0	3	19	W56172	Anti-inflammatory
14	9	75.0	3	20	W86037	Peptide used in th
15	9	75.0	3	21	Y51896	Biostatin TR232 sy
16	9	75.0	4	2	P10138	Sequence of antiln
17	9	75.0	4	2	P10093	Sequence of peptid
18	9	75.0	4	2	P10382	Enkephalin-like an
19	9	75.0	4	3	P20217	Analgesic and neur
20	9	75.0	4	4	P30083	Sequence of chromo
21	9	75.0	4	4	P30085	Sequence of cyclic
22	9	75.0	4	5	P40538	Sequence of cyclic
23	9	75.0	4	5	P40539	Sequence of cyclic
24	9	75.0	4	8	P70833	Sequence encoded b
25	9	75.0	4	10	P91661	Synthetic peptide
26	9	75.0	4	12	R11077	Peptide fragment #
27	9	75.0	4	12	R11079	Peptide fragment #
28	9	75.0	4	12	R11508	Thioredoxin active
29	9	75.0	4	12	R11744	Cyclic platelet ag
30	9	75.0	4	12	R11745	Cyclic platelet ag
31	9	75.0	4	12	R12554	Ocular pressure re
32	9	75.0	4	12	R13935	Antibiotic PR90137
33	9	75.0	4	12	R14723	Farnesyl-protein t
34	9	75.0	4	12	R15751	Farnesyl-protein t
35	9	75.0	4	12	R15752	Farnesyl-protein t
36	9	75.0	4	12	R15753	Farnesyl-protein t
37	9	75.0	4	12	R15754	Farnesyl-protein t
38	9	75.0	4	12	R15755	Farnesyl-protein t
39	9	75.0	4	12	R15756	Farnesyl-protein t
40	9	75.0	4	12	R15757	Farnesyl-protein t
41	9	75.0	4	12	R15758	Farnesyl-protein t
42	9	75.0	4	12	R15759	Farnesyl-protein t
43	9	75.0	4	12	R15760	Farnesyl-protein t
44	9	75.0	4	12	R15761	Farnesyl-protein t
45	9	75.0	4	21	Y80840	Fluorophore-label

ALIGNMENTS

```
RESULT 1
P10301
ID P10301 standard; Protein; 3 AA.
XX
AC P10301;
DT 19-AUG-1992 (first entry)
XX
DE Sequence which corresp. to residues 19-21 of insulin A chain.
XX
KW Cystine peptide; insulin activity; hormone; diabetes therapy;
KW antidiabetic agent.
XX
OS Mammal.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2
FT /note= "bonded to Cys(5) of P10115, which is
FT residue 19 of the B chain fragment
FT B15-27"
XX
PN DD147942-A.
XX
PD 29-APR-1981.
XX
PF 01-FEB-1980; 80DD-0011868.
XX
PR 20-AUG-1979; 79DD-0215100.
XX
PA (LOSS/) LOSSE G.
XX
PI Losse G, Stange H;
XX
DR WPI; 1981-53498D/30 (53498D).
```

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments
XX of insulin A and B chains
PS Claim 1; Page 10; 11pp; German.
XX
CC The inventors claim the prepn. of new cysteine peptides with insulin-
CC like activity. The new peptides comprise a sequence with corresp. to
CC a central portion of the insulin B chain (esp. B15-27) and a
CC cysteine-contg. peptide with an AA sequence corresp. to a terminal
CC portion of the insulin A chain (esp. A1-7). The new cysteine
CC peptides are antidiabetic agents with appreciable insulin activity
CC (lower than that of insulin itself) and low antigenic activity.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
I
Db 2 c 2

RESULT 2
P90982 ID P90982 standard; peptide; 3 AA.
XX
AC P90982;
XX
DT 06-JUN-1990 (first entry)
XX
DE Binding receptor with selectivity for a target ligand, borne by
DE an article for inactivating toxic materials.
XX
KW Toxic material; inactivator; organophosphorous cpds.; nerve poison;
KW pesticide; decontaminant; military.
XX
PN WO8902920-A.
XX
PD 06-APR-1989.
XX
PF 04-OCT-1988; 88WO-US03422.
XX
PR 05-OCT-1987; 87US-0105312.
XX
PA (LITT) LITTLE AD INC.
XX
PI Taylor RF;
XX
DR WPI; 1989-114395/15.
XX
PT Article for inactivating toxic materials, eg organo:phosphorous cpds. -
PT comprises solid carrier bearing target ligand binding receptor
PT and ligand-degrading receptor, pref. enzyme
XX
PS Claim 7a; page 42; 57pp; English.
XX
CC The article for inactivating a toxic material comprises a solid carrier
CC bearing a first receptor which binds the target ligand and a second
CC receptor which degrades the target ligand. This synthetic peptide is
CC a preferred first receptor. The article may be used for covering
CC surfaces to protect or decontaminate the surface. The article is esp. for
CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg
CC pesticides and nerve poisons, bacteria and viruses, in environmental,
CC chemical, military and industrial settings.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;

QY 3 C 3
I
Db 3 c 3

RESULT 4
R34022 ID R34022 standard; peptide; 3 AA.
XX
AC R34022;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
I
Db 2 c 2

RESULT 3
P91660 ID P91660 standard; protein; 3 AA.
XX
AC P91660;
XX
DT 29-JUN-1990 (first entry)
XX
DE Synthetic peptide corresp. to residues 12-14 of naturally occurring
DE epidermal growth factor (EGF).
XX
KW Epidermal growth factor; angiogenesis; synthetic peptide.
XX
FH Key
FT Misc-difference 1 Location/Qualifiers
ET /label=OTHER
FT /note="H-Gly"
FT Misc-difference 3 /label=OTHER
FT /note="(aceto amido methyl) NH2-Cys"
XX
PN WO8901489-A.
XX
PD 23-FEB-1989.
XX
PF 10-AUG-1988; 88WO-AU00300.
XX
PR 10-AUG-1987; 87AU-0003629.
XX
PA (CSIR) COMMONWEALTH SCIENT ORG.
XX
PI MCAuslan BR;
XX
DR WPI; 1989-068852/09.
XX
PT Synthetic peptide active in stimulating angiogenesis -
PT has sequences corresponding to amino acid sequences occurring in
PT epidermal growth factor.
XX
PS Claim 3; page 10; 11pp; English.
XX
CC The inventors claim synthetic peptides which correspond to sequences
CC occurring in EGF, but excluding EGF. The peptides are angiogenic
CC and have corresp. applications, eg for the healing of wounds and
CC burns. Their relative shortness means that they pose fewer synthesis
CC problems than the entire EGF molecule. They can be admin. singly or
CC association with each other or in association with an angiogenic
CC stimulator.
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
I
Db 3 c 3

RESULT 4
R34022 ID R34022 standard; peptide; 3 AA.
XX
AC R34022;

XX 19-MAY-1993 (first entry)
XX Metal trapping peptide intermediate.
DE Electrostatic interaction; metalloprotein; binding site;
KW protecting group.
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 2 /note= "Boc protected"
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH of cysteine"
FT Modified-site 3 /note= "OME protected"
FT
FT
PN JP04346999-A.
XX
XX
PD 02-DEC-1992.
XX
PF 24-MAY-1991; 91JP-0120196.
XX
PR 24-MAY-1991; 91JP-0120196.
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
PA
DR WPI; 1993-021449/03.
XX
XX New acyclic peptide with metal trapping activity - exhibits in vivo metal transporting action and can be used as drug, diagnostic agent or functional material
PS Claim 3; Page 2; 9pp; Japanese.
XX
CC The acyclic peptide (see R31340) with metal trapping activity may be produced by fragment condensation using the peptide fragments given in R34022-29.
CC
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 2 C 2

RESULT 5
R34023
ID R34023 standard; peptide; 3 AA.
XX
AC R34023;
XX
XX 19-MAY-1993 (first entry)
XX
DE Metal trapping peptide intermediate.
XX
KW Electrostatic interaction; metalloprotein; binding site;
KW protecting group.
XX Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1 /note= "HCl.H-Val"
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH of cysteine"

FT Modified-site 3 /note= "OME protected" of cysteine"
FT
XX
PN JP04346999-A.
XX
PD 02-DEC-1992.
XX
PF 24-MAY-1991; 91JP-0120196.
XX
PR 24-MAY-1991; 91JP-0120196.
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
PA
DR WPI; 1993-021449/03.
XX
XX New acyclic peptide with metal trapping activity - exhibits in vivo metal transporting action and can be used as drug, diagnostic agent or functional material
PS Claim 3; Page 2; 9pp; Japanese.
XX
CC The acyclic peptide (see R31340) with metal trapping activity may be produced by fragment condensation using the peptide fragments given in R34022-29.
CC
XX
SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 2 C 2

RESULT 6
R51439
ID R51439 standard; peptide; 3 AA.
XX
AC R51439;
XX
XX 27-OCT-1994 (first entry)
XX
DE IGF-1 analogue N-terminal.
XX
KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg; in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
XX
OS Homo sapiens.
XX
PN WO9406445-A.
XX
PD 31-MAR-1994.
XX
PF 02-SEP-1993; 93WO-US08279.
XX
PR 17-SEP-1992; 92US-0947035.
XX (EMBR-) EMBREX INC.
PA (GROP-) GROPEP PTY LTD.
PA (USDA) US SEC OF AGRIC.
XX
PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
PI Walton PE;
XX
DR WPI; 1994-118144/14.
XX
XX Increasing growth of birds - with insulin-like growth factor delivered to the egg before hatching esp. for increasing wt. gain in chickens.
PT

XX Claim 6; Page 37; 45pp; English.
 XX Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3
 CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 Db 3 C 3

RESULT 7
 R51440
 ID R51440 standard; peptide; 3 AA.
 AC R51440;
 XX
 XX 27-OCT-1994 (first entry)
 DE IGF-1 analogue N-terminal.
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 XX Homo sapiens.
 OS
 XX WO9406445-A.
 PN 31-MAR-1994.
 PD 02-SEP-1993; 93WO-US08279.
 PF 17-SEP-1992; 92US-0947035.
 PR (EMBR-) EMBREX INC.
 XX (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 PI WPI; 1994-118144/14.
 DR Increasing growth of birds - with insulin-like growth factor
 XX delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.
 XX Claim 6; Page 37; 45pp; English.
 PS Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3

XX weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.
 CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX Sequence 3 AA;
 SQ

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 Db 3 C 3

RESULT 8
 R51441
 ID R51441 standard; peptide; 3 AA.
 XX
 AC R51441;
 XX
 XX 27-OCT-1994 (first entry)
 DE IGF-1 analogue N-terminal.
 XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
 KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
 XX Homo sapiens.
 OS
 XX WO9406445-A.
 PN 31-MAR-1994.
 PD 02-SEP-1993; 93WO-US08279.
 PF 17-SEP-1992; 92US-0947035.
 PR (EMBR-) EMBREX INC.
 XX (GROP-) GROPEP PTY LTD.
 PA (USDA) US SEC OF AGRIC.
 XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
 PI Walton PE;
 PI WPI; 1994-118144/14.
 DR Increasing growth of birds - with insulin-like growth factor
 XX delivered to the egg before hatching esp. for increasing wt. gain
 PT in chickens.
 XX Claim 6; Page 37; 45pp; English.
 PS Growth of birds is increased by (a) admin. to the bird, in ovo,
 CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;
 CC (b) incubating to hatch and (c) growing the birds for at least 3
 CC weeks after hatch.
 CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or
 CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,
 CC partic. Gly and the Thr normally adjacent to Glu can be replaced
 CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal
 CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 Db 3 c 3

RESULT 9
 W19847
 ID W19847 standard; Peptide; 3 AA.
 XX
 AC W19847;
 XX
 XX 23-SEP-1997 (first entry)
 DT
 DE Human interleukin-12 p40 subunit N-terminal peptide.

XX
 KW Interleukin-12; FC gamma-1; immunosuppressive; autoimmune disease;
 KW graft rejection; toxic shock; therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09720062-AL.
 XX
 PD 05-JUN-1997.
 XX
 PF 02-DEC-1996; 96WO-US19181.
 PR
 PR 01-DEC-1995; 95US-0565856.
 XX
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 PA (UYMA-) UNIV MASSACHUSETTS.
 PI Steel AW, Strom TB;
 XX
 DR WPI; 1997-310615/28.
 DR N-PSDB; T72095-96.
 XX

PT Fusion protein containing interleukin-12 p40 subunit - has
 PT increased stability, used to inhibit graft rejection, or treat
 PT autoimmune disease and endotoxin-induced shock
 XX
 PS Example; Fig 2; 36pp; English.
 XX
 CC A peptide (W19847) comprises the three N-terminal amino acid
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is
 CC encoded both by native human p40 cDNA (T72096) and by a primer
 CC (T72095) based on the native sequence. PCR amplification has
 CC been used to amplify p40 cDNA. A fusion protein comprising the
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed
 CC in E. coli. This fusion protein has a longer in vivo half-life
 CC than native p40 and can be used as an immunosuppressive (e.g. to
 CC treat autoimmune diseases or to inhibit graft rejection) or to
 CC treat or prevent endotoxin-induced shock.

XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 C 3
 Db 2 c 2

RESULT 10
 W56231
 ID W56231 standard; peptide; 3 AA.
 XX
 AC W56231;
 XX

DT 20-JUL-1998 (first entry)
 DE Anti-inflammatory tripeptide.
 XX

KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
 KW T-cell inhibitory activity; adherence; extracellular matrix;
 KW up-regulation; fas receptor expression; inflammation.

XX Synthetic.
 XX
 PN W09809985-A2.
 XX
 PD 12-MAR-1998.
 XX
 PF 03-SEP-1997; 97WO-IL00295.
 XX
 PR 28-MAY-1997; 97US-0864301.
 PR 03-SEP-1996; 96US-0025376.
 PR 20-NOV-1996; 96US-0753141.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.

XX
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
 XX
 DR WPI; 1998-193550/17.

PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease

XX Claim 7; Page 33; 42pp; English.

XX
 CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:

CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
 CC Xaa = any amino acid residue.

CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 Db 3 c 3

```

RESULT 11
W56211
ID W56211 standard; peptide; 3 AA.
XX AC W56211;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN WO9809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX PA Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX PI WPI; 1998-193550/17.
XX DR
XX PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX PS Claim 6; Page 35; 42pp; English.
XX CC W56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be used
CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;
Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 C 3
DB 1 C 1
RESULT 12
W56200
ID W56200 standard; peptide; 3 AA.
XX AC W56200;
XX DT 20-JUL-1998 (first entry)

```

```

XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN WO9809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX PA Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX PI WPI; 1998-193550/17.
XX DR
XX PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX PS Claim 5; Page 34; 42pp; English.
XX CC W56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be used
CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;
Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 C 3
DB 3 C 3
RESULT 13
W56172
ID W56172 standard; peptide; 3 AA.
XX AC W56172;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX

```

OS Synthetic.
 PN WO9809985-A2.
 XX
 PD 12-MAR-1998.
 XX
 PF 03-SEP-1997; 97WO-IL00295.
 XX
 PR 28-MAY-1997; 97US-0864301.
 PR 03-SEP-1996; 96US-0025376.
 PR 20-NOV-1996; 96US-0753141.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
 XX
 DR WPI; 1998-193550/17.
 XX
 PT Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease
 XX
 PS Claim 3; Page 34; 42pp; English.
 XX
 CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
 CC Xaa = any amino acid residue.
 CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 C 3
 Db 1 c 1

RESULT 14
 W88037
 ID W88037 standard; peptide; 3 AA.
 AC W88037;
 XX
 DT 09-APR-1999 (first entry)
 XX
 DE Peptide used in the hair composition of the invention.
 XX
 KW Hair; styling; wave.
 XX
 XX Synthetic.
 OS
 PN JP11012138-A.
 XX
 PD 19-JAN-1999.
 XX
 PF 18-JUN-1997; 97JP-0161657.
 XX

PR 18-JUN-1997; 97JP-0161657.
 XX
 PA (LIOY) LION CORP.
 XX
 DR WPI; 1999-148442/13.
 XX
 PT New composition for hair - comprises oligopeptide having more than 2
 PT cysteine residues and reducing agent
 XX
 PS Example 2; Page 6; 17pp; Japanese.
 XX
 CC Peptides W88033-39 are used in the hair composition of the invention.
 CC The specification describes a hair composition that comprises at
 CC least one oligopeptide having more than two cysteine residues and more
 CC than three amino acid residues of the same kind (except cysteine) and a
 CC reducing agent. The composition is useful for styling hair to take
 CC various shapes and waves safely and effectively.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 20; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 C 3
 Db 1 c 1

RESULT 15
 Y51896
 ID Y51896 standard; peptide; 3 AA.
 AC Y51896;
 XX
 DT 16-JUN-2000 (first entry)
 XX
 DE Biostatin TT232 synthesising peptide 1.
 XX
 KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;
 KW cellular proliferation inhibition; somatostatin; antitumor.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "TFA*Lys(2)"
 FT Modified-site 2 /note= "Cys(Acm)"
 FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"
 FT
 XX WO200011032-A2.
 PN
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-EP06131.
 XX
 PR 20-AUG-1998; 98WO-EP05306.
 XX
 PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.
 XX
 PI Braun G, Lifferth A, Birr C;
 XX
 DR WPI; 2000-224663/19.
 XX
 PT Biostatin preparation in high yield by solid synthesis, including
 PT closure of disulfide bridge before cleavage from support, useful as
 PT antitumor agent -
 XX
 PS Example 4; Page 23; 33pp; German.
 XX

CC This invention describes a novel method for the solid phase (SP)
 CC synthesis of biostatin (TT 232) (I) which includes closing the disulfide
 CC bridge by oxidation of the completely or partially constructed peptide
 CC while still bonded to the solid phase. The products of the invention have
 CC cytostatic activity and are tyrosine kinase inhibitors. (I) inhibits the
 CC tyrosine kinase activity of various human stomach cancer cell lines and
 CC thus inhibits cellular proliferation. The heptapeptide (I) described in
 CC the invention is a somatostatin analog which shows strong antitumor
 CC activity in vitro and in vivo. The SP synthesis method gives (I) is more
 CC easily and in markedly higher yield than by the method of EP505680, in
 CC which the cyclization is carried out after cleaving the peptide from the
 CC resin. The solution method is also a simple synthesis of (I) in high
 CC yield; typically the tert-butyl-protected precursor can be oxidized in
 CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the
 CC synthesis of biostatin TT232 described in the method of the invention.

XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 2 c 2

Search completed: February 5, 2001, 12:01:19
 Job time: 366 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:53 ; Search time 30.91 Seconds
(without alignments)
2.324 Million cell updates/sec

Title: US-09-687-267-5

Perfect score: 12

Sequence: 1 XXCX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/iaa/PCTRUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-386-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-399-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	3	1	US-07-791-213D-22
22	9	75.0	3	1	US-07-791-213D-38
23	9	75.0	3	1	US-07-945-982-2
24	9	75.0	3	1	US-07-945-982-8
25	9	75.0	3	1	US-07-947-035-3
26	9	75.0	3	1	US-07-947-035-4
27	9	75.0	3	1	US-07-947-035-5
28	9	75.0	3	1	US-08-285-443-4

29 9 75.0 3 1 US-08-079-812-31 Sequence 31, Appl
30 9 75.0 3 1 US-08-122-510-11 Sequence 11, Appl
31 9 75.0 3 1 US-08-122-510-12 Sequence 12, Appl
32 9 75.0 3 1 US-08-122-510-13 Sequence 13, Appl
33 9 75.0 3 1 US-07-789-913-26 Sequence 26, Appl
34 9 75.0 3 1 US-08-371-930-4 Sequence 4, Appl
35 9 75.0 3 1 US-08-049-794-26 Sequence 26, Appl
36 9 75.0 3 1 US-08-372-455-2 Sequence 2, Appl
37 9 75.0 3 1 US-08-372-455-8 Sequence 8, Appl
38 9 75.0 3 1 US-08-321-585A-1 Sequence 1, Appl
39 9 75.0 3 1 US-08-321-585A-2 Sequence 2, Appl
40 9 75.0 3 1 US-08-321-585A-3 Sequence 3, Appl
41 9 75.0 3 1 US-08-446-908-14 Sequence 14, Appl
42 9 75.0 3 1 US-08-231-205A-14 Sequence 14, Appl
43 9 75.0 3 1 US-08-293-150A-22 Sequence 22, Appl
44 9 75.0 3 1 US-08-293-150A-38 Sequence 38, Appl
45 9 75.0 3 3 US-08-447-515-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-07-791-213D-23

; Sequence 23, Application US/07791213D

; Patent No. 5409895

; GENERAL INFORMATION:

; APPLICANT: MORISHITA, Hideaki

; APPLICANT: KANAMORI, Toshinori

; APPLICANT: NOBUHARA, Masahiro

; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE

; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME

; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF

; TREATING USING THE SAME

; NUMBER OF SEQUENCES: 108

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07791,213D

; FILING DATE: 13-NOV-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 2-306745

; FILING DATE: 13-NOV-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Meuth, Donna M

; REGISTRATION NUMBER: 36,607

; REFERENCE/DOCKET NUMBER: 029650-032

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

RESULT 5
US-08-461-838-9
; Sequence 9, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
; US-08-461-838-9

; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

RESULT 6
US-08-293-150A-23
; Sequence 23, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NORUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-5620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 2 C 2

RESULT 7
US-08-293-150A-39
; Sequence 39, Application US/08293150A
```


Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 1 C 1

RESULT 8
US-08-461-386-9
Sequence 9, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..2
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 2 C 2

RESULT 9
US-08-465-380-307
Sequence 307, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Berghum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/268
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; OTHER INFORMATION: amino acid.
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 10
US-08-486-397-307
; Sequence 307, Application US/08486399
; Patent No. 5866542
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 357
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,397
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/269
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; OTHER INFORMATION: amino acid.
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 11
US-08-486-399-307
; Sequence 307, Application US/08486399
; Patent No. 5866543
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,399
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; OTHER INFORMATION: amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 1 C 1

RESULT 12

US-08-461-965-307
; Sequence 307, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 1 C 1

RESULT 13

US-08-634-641-307
; Sequence 307, Application US/08634641
; Patent No. 5955294
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George P. Vlasuk
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Mensens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,641
; FILING DATE: April 19, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

RESULT 14

US-08-818-253-52
; Sequence 52, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-818-253-52

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

RESULT 15

US-09-249-471-307
; Sequence 307, Application US/09249471
; Patent No. 604041
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,471
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: Internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; OTHER INFORMATION: amino acid.
US-09-249-471-307

Query Match 75.0%; Score 9; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

Search completed: February 5, 2001, 12:01:54
Job time: 336 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:02:32 ; Search time 34.92 Seconds
(without alignments)
7.778 Million cell updates/sec

Title: US-09-687-267-5

Perfect score: 12

Sequence: 1 XXCX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	75.0	3	2	R-phycoerythrin al
2	9	75.0	4	2	metallothionein-A
3	9	75.0	4	2	Ig mu chain V regi
4	9	75.0	4	2	pallidipin - assas
5	9	75.0	5	2	R-phycoerythrin al
6	9	75.0	5	2	R-phycoerythrin ga
7	9	75.0	5	2	cadmium-binding pe
8	9	75.0	5	2	actin I - malaria
9	9	75.0	5	2	hemoglobin, extrac
10	9	75.0	5	2	lipopeptide WS1279
11	9	75.0	6	2	R-phycoerythrin be
12	9	75.0	6	2	protamine p1 - gor
13	9	75.0	6	2	Y protein - human
14	9	75.0	6	2	Na+/K+-exchanging
15	9	75.0	6	2	glycoprotein compo
16	9	75.0	6	2	MHC H2-K-k cell su
17	9	75.0	6	2	MHC H2-L antigen -
18	9	75.0	6	2	T-cell receptor be
19	9	75.0	6	2	F41946
20	9	75.0	6	2	laminin B1 - weste
21	9	75.0	6	4	hypothetical TGL3
22	9	75.0	7	2	Ig heavy chain V r
23	9	75.0	7	2	venom heptapeptide
24	9	75.0	7	2	S08606
25	9	75.0	7	2	hypothetical prote
26	9	75.0	7	2	mablinin ii chain
27	9	75.0	7	2	vicilin 57K chain
28	9	75.0	7	2	cadmium-binding he
29	9	75.0	7	2	acetylcholinestera
					formylglycinamide

30	9	75.0	7	2	PH1602	Ig H chain V-D-J r
31	9	75.0	7	2	PH0932	T-cell receptor be
32	9	75.0	7	4	I56695	hypothetical I2 pr
33	9	75.0	8	2	PH1407	Ig heavy chain V r
34	9	75.0	8	2	S59622	metallothionein is
35	9	75.0	8	2	XGHUEU	urine glycopeptide
36	9	75.0	8	2	A25836	L-serine dehydrata
37	9	75.0	8	2	PCI002	leucine--trna liga
38	9	75.0	8	2	S19288	acylase - Kluuvera
39	9	75.0	8	2	A37521	R-phycoerythrin ga
40	9	75.0	8	2	C61512	variant surface gl
41	9	75.0	8	2	D61512	variant surface gl
42	9	75.0	8	2	PH1618	Ig H chain V-D-J r
43	9	75.0	8	2	PH0803	T-cell receptor al
44	9	75.0	8	2	I57018	gene Cfr protein
45	9	75.0	8	2	PH0934	T-cell receptor be

ALIGNMENTS

RESULT 1

A22565

R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C>Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993

C:Accession: A22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601

A:Accession: A22565

A:Molecule type: protein

A:Residues: 1-3 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 1 C 1

RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: I51049

R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; MUID:95324545

A:Accession: I51049

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <OLS>

A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3

Db 4 C 4

RESULT 3

S43959

Ig mu chain V region (clone 13) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 2 C 2

RESULT 4
S55238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S55238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuning
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib
A:Reference number: S55238; MUID:95251610
A:Accession: S55238
A:Molecule type: protein
A:Residues: 1-4 <HAE>

Query Match 75.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 3 C 3

RESULT 5
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: B22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: B22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 2 C 2

RESULT 6
F22565

R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: F22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: F22565
A:Molecule type: protein
A:Residues: 1-5 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 3 C 3

RESULT 7
A33882
cadmium-binding pentapeptide - downy thornapple
C:Species: Datura innoxia (downy thornapple)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C:Accession: A33882
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A:Title: Poly(gamma-glutamylcysteinylglycine: its role in cadmium resistance in plan
A:Reference number: A94182; MUID:88016144
A:Accession: A33882
A:Molecule type: protein
A:Residues: 1-5 <JAC>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 2 C 2

RESULT 8
B45525
actin I - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C:Accession: B45525
R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen
Mol. Biochem. Parasitol. 35, 167-176, 1989
A:Title: Stage-specific expression and genomic organization of the actin genes of the
A:Reference number: A45525; MUID:89364996
A:Accession: B45525
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <WES>
A:Cross-references: GB:J03988
A:Note: the authors translated the codon GAA for residue 3 as Gly
C:Comment: The actin I gene contains no introns.

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 4 C 4

RESULT 9
S65726
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
C:Species: Lumbricus terrestris (common earthworm)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65726
R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobin
A:Reference number: S65721; MUID:96176855
A:Accession: S65726
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <FUS>

Query Match 75.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
DB 4 C 4

RESULT 10
JU0355
lipopeptide WS1279 [validated] - Streptomyces willmorei
C:Species: Streptomyces willmorei
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: JU0355
R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
Chem. Pharm. Bull. 39, 607-611, 1991
A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin
A:Reference number: JU0355; MUID:91300586
A:Accession: JU0355
A:Molecule type: protein
A:Residues: 1-6 <TSU>
A:Note: the structure was confirmed by synthesis
C:Keywords: blocked amino end; lipoprotein
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
DB 1 C 1

RESULT 11
C22565
R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: C22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: C22565
A:Molecule type: protein
A:Residues: 1-6 <KLO>

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
DB 1 C 1

RESULT 12
I37027
protamine P1 - gorilla (fragment)
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-
A:Reference number: I37013; MUID:94040810
A:Accession: I37027
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
DB 6 C 6

RESULT 13
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative
A:Reference number: I37263; MUID:93010691
A:Accession: I37263
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
DB 4 C 4

RESULT 14
S29881
Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S29881
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases arou
A:Reference number: S29881; MUID:85131201
A:Accession: S29881
A:Molecule type: protein
A:Residues: 1-6 <WAL>
A:Experimental source: kidney

C;Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status Predicted

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 2 C 2

RESULT 15

H48394
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576
A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Experimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein

Query Match 75.0%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 6 C 6

Search completed: February 5, 2001, 12:02:32
Job time: 289 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:06:02 ; Search time 20.72 Seconds
(without alignments)
6.234 Million cell updates/sec

Title: US-09-687-267-5
Perfect score: 12
Sequence: 1 XXCX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	75.0	8	ACT_CARMA	P80709 carcinus ma
2	9	75.0	8	GLUR_HUMAN	P02729 homo sapien
3	9	75.0	9	CCAP_CARMA	P38556 carcinus ma
4	9	75.0	9	CONO_CONGE	P05486 conus geogr
5	9	75.0	9	CONO_CONST	P05487 conus stria
6	9	75.0	9	DNF1_LOCM1	P16339 locusta mig
7	9	75.0	9	ISOT_CYPCA	P42993 cyprinus ca
8	9	75.0	9	MGMT_BOVIN	P29177 bos taurus
9	9	75.0	9	OXVA_SCYCA	P42996 scyllorhinu
10	9	75.0	9	OXVA_SQUAC	P42999 squallus aca
11	9	75.0	9	OXFE_SCYCA	P42997 scyllorhinu
12	9	75.0	9	OXIT_BUFRE	P42995 bufo regula
13	9	75.0	9	OXYT_CYPCA	P23879 cyprinus ca
14	9	75.0	9	OXYT_EISFO	P42998 eisenia foe
15	9	75.0	9	OXYT_OCTUV	P80027 octopus vul
16	9	75.0	9	OXYT_RABIT	P32878 oryctolagus
17	9	75.0	9	OXYT_RAJCL	P42994 raja clavav
18	9	75.0	9	OXIV_SQUAC	P43000 squallus aca
19	9	75.0	9	RS11_SALTY	O54296 salmonella
20	9	75.0	9	SAP_STOVA	P24047 stomopneute
21	9	75.0	9	TAL1_PICJA	P17440 pichia jadi
22	9	75.0	9	TAL3_PICJA	P17441 pichia jadi
23	9	75.0	10	GLEM_HUMAN	P02728 homo sapien
24	9	75.0	10	GON2_CHEPR	P80678 chelyosoma
25	9	75.0	10	RCA_FINPS	P81084 pinus pinas
26	9	75.0	12	CXA1_CONIM	P50983 conus imper
27	9	75.0	12	NO40_LOTJA	O22426 lotus japon
28	9	75.0	12	NO40_SESRO	O24369 sesbania ro
29	9	75.0	12	NO40_SOYBN	P55960 glycine max
30	9	75.0	12	R116_GINBI	P36207 ginkgo bilo
31	9	75.0	12	TAL10_TREME	P01371 tremella me
32	9	75.0	12	UR2A_CATCO	P04558 catostomus
33	9	75.0	12	UR2B_CATCO	P04559 catostomus

34 9 75.0 12 1 UR2B_CYPCA P04561 cyprinus ca
35 9 75.0 12 1 UR2_GILMI P01147 gillichthys
36 9 75.0 12 1 UR2_POLSP P81022 polyodon sp
37 9 75.0 12 1 UR2_SCYCA P35490 scyllorhinu
38 9 75.0 12 1 YZPY_ECOLI P17776 escherichia
39 9 75.0 13 1 ACT7_SOYBN P15987 glycine max
40 9 75.0 13 1 CXAL_CONST P15471 conus stria
41 9 75.0 13 1 CXA2_CONGE P01520 conus stria
42 9 75.0 13 1 CXAA_CONST P28878 conus stria
43 9 75.0 13 1 CXET_CONTE P81755 conus texti
44 9 75.0 13 1 GER1_HORVU P28525 hordeum vul
45 9 75.0 13 1 GER2_HORVU P28526 hordeum vul

ALIGNMENTS

RESULT 1
ACT_CARMA
ID ACT_CARMA STANDARD; PRT; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN (FRAGMENT).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
RA Baghdassarian D.; An enzyme implicated in crab steroidogenesis.";
RT "A transalcolase.
RL Endocrine 5:23-32(1996).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 6.8, ITS MW IS: 46 KDA.
CC -!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
DR INTERPRO; IPR000279;
DR PROSITE; PS00406; ACTINS_1; PARTIAL.
DR PROSITE; PS00432; ACTINS_2; PARTIAL.
DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
KW Structural protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 2 C 2

RESULT 2
GLUR_HUMAN
ID GLUR_HUMAN STANDARD; PRT; 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE URINE GLYCOPETIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]

RP SEQUENCE
RX MEDLINE=72062338; PubMed=5126885;
RA Lote C.J., Weiss J.B.;
RT "Identification in urine of a low-molecular-weight highly polar
RT glycopeptide containing cysteinyl-galactose.";
RL Biochem J. 123:25p-25p(1971).
CC -!- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPOLYPEPTIDE HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
DR PIR: A03188; XGHUEU.
KW Glycoprotein.
FT CARBOHYD
SQ SEQUENCE 8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;

Query Match 75.0%; Score 9; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 3
CCAP_CARMA STANDARD; PRT; 9 AA.
ID CCAP_CARMA
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CARDIOACTIVE PEPTIDE (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
RN [1]
RP SEQUENCE.
RC SPECIES=C. MAENAS; TISSUE=PERICARDIAL ORGANS;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M. SEXTA;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylvester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T. MOLITOR, AND S. ERIDANIA; TISSUE=HEAD;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuoya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYPH.
DR PIR: A26363; A26363.
KW Neuropeptide; Amidation.
FT MOD_RES 3 9
FT SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 4
CONO_CONGE STANDARD; PRT; 9 AA.
ID CONO_CONGE
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE LYS-CONOPRESSIN G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: A28495; A28495.
DR INTERPRO: IPR000981;
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 5
CONO_CONST STANDARD; PRT; 9 AA.
ID CONO_CONST
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ARG-CONOPRESSIN S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus straitus venoms.*;
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]

RP REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.*;
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; B28495; B28495.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 1 C 1

RESULT 6
 DNFI_LOCFMI STANDARD; PRT; 9 AA.
 AC P16339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE LOCUPRESSIN (DIURETIC NEUROPEPTIDE FI/F2).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridomorpha; Acridoidea; Acrididae; Locusta.
 RN [1]

RP SEQUENCE.
 RC TISSUE=SUBESOPHAGEAL GANGLION, AND THORACIC GANGLION;
 RX MEDLINE=88077077; PubMed=3689410;
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
 RA Delaage M., Schooley D.A.;
 RT "Identification of an arginine vasopressin-like diuretic hormone from
 RL Locusta migratoria.*;
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
 CC -!- FUNCTION: DIURETIC HORMONE.
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR; A29477; A29477.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT DISULFID 1 6
 FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
 FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 1 C 1

RESULT 7
 ISOT_CYPCA STANDARD; PRT; 9 AA.
 AC P42993;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE ISOTOCIN.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 RN [1]

RP SEQUENCE.
 RC TISSUE=PIUITARY;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony
 fish, the carp (Cyprinus carpio). Comparison with hormones from sea
 water bony fish.*;
 RL Comp. Biochem. Physiol. 14:245-254(1965).
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A61364; A61364.
 DR INTERPRO: IPR000981; -.
 DR PFAM: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 1 C 1

RESULT 8
 MGMT_BOVIN STANDARD; PRT; 9 AA.
 AC P29177;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63) (6-O-
 DE METHYLGUANINE-DNA METHYLTRANSFERASE) (FRAGMENT).
 GN MGMT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]

RP SEQUENCE.
 RC TISSUE=THYMUS;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B., Hall J., Karan P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 methyltransferase.*;
 RL Nucleic Acids Res. 18:17-21(1990).
 CC -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
 TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
 RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
 IRREVERSIBLY INACTIVATED
 CC -!- CATALYTIC ACTIVITY: DNA (CONTAINING O6-METHYLGUANINE) + PROTEIN
 L-CYSTEINE -> DNA (WITHOUT O6-METHYLGUANINE) + PROTEIN S-METHYL-
 L-CYSTEINE.
 CC -!- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE
 WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
 DR INTERPRO: IPR001497; -.

Query Match 75.0%; Score 9; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 1 C 1

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DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 9
OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RA Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 10
OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ASPARTOCIN (ASPARTOCIN).
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
RN [1]
RP SEQUENCE.
RX Acher R., Chauvet J., Chauvet M.-T.;

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RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RT isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
RN [2]
RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophysial hormones, valitocin (Val9-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
CC C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB444404B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 11
OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHASVATOCIN.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=PITUITARY;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus caniculus).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT MOD_RES 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 12
OXYT_BUFRE

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ID OXYT_BUFRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE SERITOCIN.
OS Bufo regularis (African toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
OC Bufo.
RN [1]
RN SEQUENCE.
RC TISSUE=PITUITARY NEUROINTERMEDIATE LOBE;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: DEVOID OF OXYTOCIN ACTIVITY.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 13
OXYT_CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE VASOTOCIN.
OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
RN [1]
RN SEQUENCE.
RC SPECIES=C.CARPIO; TISSUE=PITUITARY;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RN SEQUENCE.
RC SPECIES=P.MARINUS; TISSUE=PITUITARY;
RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 1 C 1

RESULT 15
OXYT_OCTVU STANDARD; PRT; 9 AA.
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CEPHALOTOCIN.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
RN [1]
RN SEQUENCE.
RC TISSUE=NERVE ENDINGS;

```

RX MEDLINE=92270139; PubMed=1589145;
RA Reich G.;
RT "A new peptide of the oxytocin/vasopressin family isolated from
RT nerves of the cephalopod Octopus vulgaris.";
RL Neurosci. Lett. 134:191-194(1992).
CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
CC CAVA.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR INTERPRO: IPR000981; -.
DR PFAM: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1072 MW; 17FF476B45409DB CRC64;

Query Match 75.0%; Score 9; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 1 C 1

Search completed: February 5, 2001, 12:06:02
Job time: 279 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:05:38 ; Search time 57.72 Seconds
(without alignments)
8.123 Million cell updates/sec

Title: US-09-687-267-5
Perfect score: 12
Sequence: 1 XXCX 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL15:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	9	75.0	6	4	Q08720	Q08720 homo sapien
2	9	75.0	7	2	P70804	P70804 azotobacter
3	9	75.0	7	11	O55184	O55184 rattus norv
4	9	75.0	7	12	O66113	O66113 cherry leaf
5	9	75.0	7	12	O67113	O67113 influenza a
6	9	75.0	7	12	O9YVE3	O9YVE3 human adeno
7	9	75.0	7	12	O9YVRO	O9YVRO human adeno
8	9	75.0	7	12	O9YVIO9	O9YVig9 human adeno
9	9	75.0	7	13	O42564	O42564 fugu rubrip
10	9	75.0	8	2	O32560	O32560 escherichia
11	9	75.0	8	4	Q15888	Q15888 homo sapien
12	9	75.0	8	4	Q15890	Q15890 homo sapien
13	9	75.0	8	4	Q15900	Q15900 homo sapien
14	9	75.0	8	4	O9Y4X6	O9Y4X6 homo sapien
15	9	75.0	8	6	O02831	O02831 oryctolagus
16	9	75.0	8	6	O9TRY3	O9TRY3 sus sp. ins
17	9	75.0	8	10	O9SAY7	O9SAY7 dioscorea t
18	9	75.0	8	11	P70243	P70243 mus musculu
19	9	75.0	8	11	O35835	O35835 rattus norv

20	9	75.0	8	12	Q85562	Q85562 moloney mur
21	9	75.0	8	13	Q90493	Q90493 eopsaltria
22	9	75.0	8	13	Q90498	Q90498 erythrura g
23	9	75.0	8	13	Q91098	Q91098 manorina me
24	9	75.0	9	2	Q47063	Q47063 escherichia
25	9	75.0	9	4	O15999	O15999 homo sapien
26	9	75.0	9	4	O99887	O99887 homo sapien
27	9	75.0	9	6	Q9XT05	Q9XT05 macropus ru
28	9	75.0	9	6	O9TUY0	O9TUY0 monodelphis
29	9	75.0	9	9	Q38340	Q38340 lactococcus
30	9	75.0	9	11	P9Q2A8	P9Q2A8 mus musculu
31	9	75.0	9	11	P97889	P97889 rattus norv
32	9	75.0	9	12	O69473	O69473 human herpe
33	9	75.0	9	12	O12096	O12096 caprine art
34	9	75.0	9	12	O12098	O12098 caprine art
35	9	75.0	9	12	O12100	O12100 caprine art
36	9	75.0	9	12	O12102	O12102 caprine art
37	9	75.0	9	12	O12104	O12104 caprine art
38	9	75.0	9	12	O90350	O90350 hepatitis g
39	9	75.0	10	2	Q50032	Q50032 mycobacteri
40	9	75.0	10	2	O47475	O47475 escherichia
41	9	75.0	10	2	O48469	O48469 klebsiella
42	9	75.0	10	2	Q9K343	Q9K343 escherichia
43	9	75.0	10	3	Q9UVW2	Q9UVW2 schizophyll
44	9	75.0	10	4	Q13318	Q13318 homo sapien
45	9	75.0	10	4	O9UN90	O9UN90 homo sapien

ALIGNMENTS

RESULT 1

ID Q08720 PRELIMINARY; PRT; 6 AA.
AC Q08720;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010691; PubMed=1396344;
RA Waeber G., Habener J.F.;
RT "Novel testis germ cell-specific transcript of the CREB gene contains
RT an alternatively spliced exon with multiple in-frame stop codons.";
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1; -.
FT NON_TER 1
FT NON_TER 6
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
Db 4 C 4

RESULT 2

ID P70804 PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE ALGG GENE (FRAGMENT).
GN Azotobacter vinelandii.
OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=; PubMed=8830682;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A2D1AED0 CRC64;

Query Match 75.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 1 C 1

RESULT 3
O55184 PRELIMINARY; PRT; 7 AA.
AC O55184;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ORPHAN RECEPTOR TR4-NS (FRAGMENT).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=86112486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
domain.";
RL Endocrinology 137:1562-1571(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299786; PubMed=8661150;
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
RT "New variants of the human and rat nuclear hormone receptor, TR4:
expression and chromosomal localization of the human gene.";
RL Genomics 35:361-366(1996).
DR EMBL; U59454; AAB91433.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 75.0%; Score 9; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 3 C 3

RESULT 4

Q66113 PRELIMINARY; PRT; 7 AA.
AC Q66113;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus.
OX NCBI_TaxID=12615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=WALNUT;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
strain).";
RL Virus Genes 10:245-252(1995).
DR EMBL; Z34265; CAA84019.1; -.
KW Repeat.
FT NON_TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 4 C 4

RESULT 5
Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE (UDORN/72) HEMAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
KW Hemagglutinin.
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
|
Db 3 C 3

RESULT 6
Q9YVE3 PRELIMINARY; PRT; 7 AA.
AC Q9YVE3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GOMEN;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065065; AAD03662.1; -;
DR EMBL; AF065066; AAD03664.1; -;
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 6 C 6

RESULT 7
Q9YI90 PRELIMINARY; PRT; 7 AA.
AC Q9YI90;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 7a.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=85755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN T96-0620, S-1058, CL 68578;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065068; AAD03668.1; -;
DR EMBL; AF065069; AAD03669.1; -;
DR EMBL; AF065067; AAD03666.1; -;
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 6 C 6

RESULT 8
Q9YI09 PRELIMINARY; PRT; 7 AA.
AC Q9YI09;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PVI CORE PROTEIN (FRAGMENT).
GN PVI.
OS Human adenovirus type 4.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2-G 95-873, RI-67, 55142;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03659.1; -;
DR EMBL; AF065062; AAD03653.1; -;
DR EMBL; AF065063; AAD03656.1; -;
FT NON_TER 1
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 75.0%; Score 9; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 6 C 6

RESULT 9
O42564 PRELIMINARY; PRT; 7 AA.
ID O42564;
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -;
KW IONIC channel.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 75.0%; Score 9; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
DB 5 C 5

RESULT 10
O32560 PRELIMINARY; PRT; 8 AA.
ID O32560;
AC O32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DE 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE PROPHONATE KINASE (FRAGMENT).
 GN TDCD.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=W3110;
 RC STRAIN=W3110;
 RA Hesslinger C., Savers G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=W3110;
 RC STRAIN=W3110;
 RA Hesslinger C., Fairhurst S.A., Savers G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ001820; CAA04875.1; -.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

 Query Match 75.0%; Score 9; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 C 3
 Db 6 C 6

 RESULT 11
 Q15888
 ID Q15888 PRELIMINARY; PRT; 8 AA.
 AC Q15888;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE (CLONE XP15H8A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32069; AAA73878.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1068 MW; 0315A37EAB5B0763 CRC64;

 Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 C 3
 Db 5 C 5

 RESULT 12
 Q15890
 ID Q15890 PRELIMINARY; PRT; 8 AA.
 AC Q15890;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)

DE (CLONE XP19G12A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32083; AAA73880.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

 Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 C 3
 Db 4 C 4

 RESULT 13
 Q15900
 ID Q15900 PRELIMINARY; PRT; 8 AA.
 AC Q15900;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE (CLONE XP7B11A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=PLACENTA;
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
 RA Caskey C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL; L32079; AAA73890.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 931 MW; B5DDC403369AAEB1 CRC64;

 Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 C 3
 Db 2 C 2

 RESULT 14
 Q9Y4X6
 ID Q9Y4X6 PRELIMINARY; PRT; 8 AA.
 AC Q9Y4X6;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE NUCLEAR LIM INTERACTOR (FRAGMENT).
 GN NLI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
 RA Schroth A., Bodem J., Royer-Pokora B.;
 RT "Genomic structure, alternative transcripts and chromosomal
 RT localization of the human LIM domain binding protein 1 gene
 RT LDB1/NLI.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243097; CAB45408.1; -;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 767 MW; EE6EBDEB862D5B6 CRC64;

Query Match 75.0%; Score 9; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 5 C 5

RESULT 15
 O02831
 ID O02831 PRELIMINARY; PRT; 8 AA.
 AC O02831;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCB1_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96377339; PubMed=8783186;
 RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
 RA Vuorio E.;
 RT "Evidence for insufficient chondrocytic differentiation during repair
 RT of full-thickness defects of articular cartilage.";
 RL Matrix Biol. 15:39-47(1996).
 DR EMBL; S83371; AAD14433.1; -;
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 75.0%; Score 9; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 C 3
 |
 Db 4 C 4

Search completed: February 5, 2001, 12:05:38
 Job time: 289 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 5, 2001, 12:01:19 ; Search time 42.35 Seconds
(without alignments)
3.230 Million cell updates/sec

Title: US-09-687-267-6

Perfect score: 12
Sequence: 1 XXXC 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
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20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	3	2 P10301	Sequence which cor
2	9	75.0	3	10 P90982	Binding receptor w
3	9	75.0	3	10 P91660	Synthetic peptide
4	9	75.0	3	14 R34022	Metal trapping pep
5	9	75.0	3	14 R34023	Metal trapping pep
6	9	75.0	3	15 R51439	IGF-1 analogue N-t
7	9	75.0	3	15 R51440	IGF-1 analogue N-t
8	9	75.0	3	15 R51441	IGF-1 analogue N-t
9	9	75.0	3	18 W19847	Human interleukin-
10	9	75.0	3	19 W56231	Anti-inflammatory
11	9	75.0	3	19 W56211	Anti-inflammatory
12	9	75.0	3	19 W56200	Anti-inflammatory

13	9	75.0	3	19 W56172	Anti-inflammatory
14	9	75.0	3	20 W88037	Peptide used in th
15	9	75.0	3	21 P11896	Biostatin TR232 sy
16	9	75.0	4	2 P10138	Sequence of antiin
17	9	75.0	4	2 P10093	Sequence of peptid
18	9	75.0	4	2 P10382	Enkephalin-like an
19	9	75.0	4	3 P20217	Analgesic and neur
20	9	75.0	4	4 P30083	Sequence of chromo
21	9	75.0	4	4 P30085	Sequence of chromo
22	9	75.0	4	5 P40538	Sequence of cyclic
23	9	75.0	4	5 P40539	Sequence of cyclic
24	9	75.0	4	8 P70833	Sequence encoded b
25	9	75.0	4	10 P91661	Synthetic peptide
26	9	75.0	4	12 R11077	Peptide fragment #
27	9	75.0	4	12 R11079	Peptide fragment #
28	9	75.0	4	12 R11508	Thioredoxin active
29	9	75.0	4	12 R11744	Cyclic platelet ag
30	9	75.0	4	12 R11745	Cyclic platelet ag
31	9	75.0	4	12 R12554	Ocular pressure re
32	9	75.0	4	12 R13935	Antibiotic FR90137
33	9	75.0	4	12 R14723	Farnesyl-protein t
34	9	75.0	4	12 R15751	Farnesyl-protein t
35	9	75.0	4	12 R15752	Farnesyl-protein t
36	9	75.0	4	12 R15753	Farnesyl-protein t
37	9	75.0	4	12 R15754	Farnesyl-protein t
38	9	75.0	4	12 R15755	Farnesyl-protein t
39	9	75.0	4	12 R15756	Farnesyl-protein t
40	9	75.0	4	12 R15757	Farnesyl-protein t
41	9	75.0	4	12 R15758	Farnesyl-protein t
42	9	75.0	4	12 R15759	Farnesyl-protein t
43	9	75.0	4	12 R15760	Farnesyl-protein t
44	9	75.0	4	12 R15761	Farnesyl-protein t
45	9	75.0	4	21 Y80840	Fluorophore-label

ALIGNMENTS

RESULT 1
P10301
ID P10301 standard; Protein; 3 AA.
AC P10301;
XX
XX
DT 19-AUG-1992 (first entry)
XX
DE Sequence which corresp. to residues 19-21 of insulin A chain.
XX
KW Cystine peptide; insulin activity; hormone; diabetes therapy;
KW antidiabetic agent.
XX
OS Mammal.
XX
XX Key Location/Qualifiers
FT Disulfide-bond 2 /note= "bonded to Cys(5) of P10115, which is
FT residue 19 of the B chain fragment
FT B15-27"
XX
XX DD147942-A.
XX
XX 29-APR-1981.
XX
XX 01-FEB-1980; 80DD-0011868.
XX
XX 20-AUG-1979; 79DD-0215100.
XX
XX (LOSS)/ LOSSE G.
XX
XX IGF-1 analogue N-t
XX
XX IGF-1 analogue N-t
XX
XX Human interleukin-
XX
XX Anti-inflammatory
XX
XX Anti-inflammatory
XX
XX WPI; 1981-53498D/30 (53498D).

PT Cysteine peptide(s) with antidiabetic activity - contg. fragments
 XX of insulin A and B chains

XX Claim 1; Page 10; 11pp; German.

CC The inventors claim the prepn. of new cysteine peptides with insulin-
 CC like activity. The new peptides comprise a sequence with corresp. to
 CC a central portion of the insulin B chain (esp. B15-27) and a
 CC cysteine-contg. peptide with an AA sequence corresp. to a terminal
 CC portion of the insulin A chain (esp. A1-7). The new cysteine
 CC peptides are antidiabetic agents with appreciable insulin activity
 CC (lower than that of insulin itself) and low antigenic activity.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 2; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
 |
 Db 2 c 2

RESULT 2

P90982
 ID P90982 standard; peptide; 3 AA.

AC P90982;

XX 06-JUN-1990 (first entry)

DE Binding receptor with selectivity for a target ligand, borne by
 DE an article for inactivating toxic materials.

XX Toxic material; inactivator; organophosphorous cpds.; nerve poison;
 KW pesticide; decontaminant; military.

XX WO8902920-A.

XX 06-APR-1989.

XX 04-OCT-1988; 88WO-US03422.

XX 05-OCT-1987; 87US-0105312.

XX (LITT) LITTLE AD INC.

XX Taylor RF;

XX WPI; 1989-114395/15.

PT Article for inactivating toxic materials, eg organo:phosphorous cpds. -
 PT comprises solid carrier bearing target ligand binding receptor
 PT and ligand-degrading receptor, pref. enzyme

XX Claim 7a; page 42; 57pp; English.

CC The article for inactivating a toxic material comprises a solid carrier
 CC bearing a first receptor which binds the target ligand and a second
 CC receptor which degrades the target ligand. This synthetic peptide is
 CC a preferred first receptor. The article may be used for covering
 CC surfaces to protect or decontaminate the surface. The article is esp. for
 CC degrading toxic organic cpds., esp. organophosphorous cpds., (eg
 CC pesticides and nerve poisons, bacteria and viruses, in environmental,
 CC chemical, military and industrial settings.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
 |
 Db 2 c 2

RESULT 3

P91660
 ID P91660 standard; protein; 3 AA.

XX P91660;

XX 29-JUN-1990 (first entry)

DE Synthetic peptide corresp. to residues 12-14 of naturally occurring
 DE epidermal growth factor (EGF).

XX Epidermal growth factor; angiogenesis; synthetic peptide.

XX Key :Location/Qualifiers
 FT Misc-difference 1
 FT /label-OTHER
 FT /note="H-Gly"

FT Misc-difference 3
 FT /label-OTHER
 FT /note="(aceto amido methyl) NH2-Cys"

XX WO8901489-A.

XX 23-FEB-1989.

XX 10-AUG-1988; 88WO-AU00300.

XX 10-AUG-1987; 87AU-0003629.

XX (CSIR) COMMONWEALTH SCIENT ORG.

XX McAuslan BR;

XX WPI; 1989-068852/09.

PT Synthetic peptide active in stimulating angiogenesis -
 PT has sequences corresponding to amino acid sequences occurring in
 PT epidermal growth factor.

XX Claim 3; page 10; 11pp; English.

CC The inventors claim synthetic peptides which correspond to sequences
 CC occurring in EGF, but excluding EGF. The peptides are angiogenic
 CC and have corresp. applications, eg for the healing of wounds and
 CC burns. Their relative shortness means that they pose fewer synthesis
 CC problems than the entire EGF molecule. They can be admin. singly or
 CC association with each other or in association with an angiogenic
 CC stimulator.

XX Sequence 3 AA;

Query Match 75.0%; Score 9; DB 10; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
 |
 Db 3 c 3

RESULT 4

R34022
 ID R34022 standard; peptide; 3 AA.

XX R34022;

XX 19-MAY-1993 (first entry)
XX Metal trapping peptide intermediate.
XX Electrostatic interaction; metalloprotein; binding site;
KW protecting group.
XX Synthetic.
XX OS
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Boc protected"
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH
FT Modified-site 3 /note= "OME protected"
FT
XX JP04346999-A.
XX
XX 02-DEC-1992.
XX
XX 24-MAY-1991; 91JP-0120196.
XX
XX 24-MAY-1991; 91JP-0120196.
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
XX WPI; 1993-021449/03.
XX New acyclic peptide with metal trapping activity - exhibits in
XX vivo metal transporting action and can be used as drug,
XX diagnostic agent or functional material
XX Claim 3; Page 2; 9pp; Japanese.
XX
XX The acyclic peptide (see R31340) with metal trapping activity may be
CC produced by fragment condensation using the peptide fragments given in
CC R34022-29.
XX
XX Sequence 3 AA;
SQ
Query Match 75.0%; Score 9; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 C 4
Db 2 c 2
RESULT 5
R34023
ID R34023 standard; peptide; 3 AA.
XX
XX R34023;
XX
XX 19-MAY-1993 (first entry)
XX Metal trapping peptide intermediate.
XX Electrostatic interaction; metalloprotein; binding site;
KW protecting group.
XX Synthetic.
XX OS
FH Key Location/Qualifiers
FT Modified-site 1 /note= "HCl.H-Val"
FT Modified-site 2 /note= "Cys(Acm); Acm= acetamidomethyl-protected SH

FT Modified-site 3 /note= "OME protected"
FT
XX JP04346999-A.
XX
XX 02-DEC-1992.
XX
XX 24-MAY-1991; 91JP-0120196.
XX
XX 24-MAY-1991; 91JP-0120196.
XX (ICHI-) ICHIKAWA GOSEI KAGAKU KK.
XX WPI; 1993-021449/03.
XX New acyclic peptide with metal trapping activity - exhibits in
XX vivo metal transporting action and can be used as drug,
XX diagnostic agent or functional material
XX Claim 3; Page 2; 9pp; Japanese.
XX
XX The acyclic peptide (see R31340) with metal trapping activity may be
CC produced by fragment condensation using the peptide fragments given in
CC R34022-29.
XX
XX Sequence 3 AA;
SQ
Query Match 75.0%; Score 9; DB 14; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 C 4
Db 2 c 2
RESULT 6
R51439
ID R51439 standard; peptide; 3 AA.
XX
XX R51439;
XX
XX 27-OCT-1994 (first entry)
XX IGF-1 analogue N-terminal.
XX
XX Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;
XX in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.
XX Homo sapiens.
XX
XX WO9406445-A.
XX
XX 31-MAR-1994.
XX
XX 02-SEP-1993; 93WO-US08279.
XX
XX 17-SEP-1992; 92US-0947035.
XX
XX (EMBR-) EMBREX INC.
XX (GROP-) GROPEP PTY LTD.
XX (USDA) US SEC OF AGRIC.
XX
XX Ballard FJ, Francis GL, McMurtry JP, Phelps PV;
XX Walton PE;
XX WPI; 1994-118144/14.
XX
XX Increasing growth of birds - with insulin-like growth factor
XX delivered to the egg before hatching esp. for increasing wt. gain
XX in chickens.

XX Claim 6; Page 37; 45pp; English.

XX Growth of birds is increased by (a) admin. to the bird, in ovo,

CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.

CC IGF-1 analogues used pref. (1) lack 1-5 N-terminal amino acids or

CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

CC partic. Gly and the Thr normally adjacent to Glu can be replaced

CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced

CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent

CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.

CC comprises the N-terminal given in R51450-53.

CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human

CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid

CC N-terminal extension.

XX Sequence 3 AA;

SQ

Query Match 75.0%; Score 9; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

DB 3 C 3

RESULT 7

R51440

ID R51440 standard; peptide; 3 AA.

XX

AC R51440;

XX

DT 27-OCT-1994 (first entry)

XX

DE IGF-1 analogue N-terminal.

XX

KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;

KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.

XX

OS Homo sapiens.

XX

PN W09406445-A.

XX

PD 31-MAR-1994.

XX

PF 02-SEP-1993; 93WO-US08279.

XX

PR 17-SEP-1992; 92US-0947035.

XX

XX (EMBR-) EMBREX INC.

PA (GROP-) GROPEP PTY LTD.

PA (USDA) US SEC OF AGRIC.

XX

PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;

PI Walton PE;

XX

XX WPI; 1994-118144/14.

XX

XX Increasing growth of birds - with insulin-like growth factor

PT delivered to the egg before hatching esp. for increasing wt. gain

PT in chickens.

XX

PS Claim 6; Page 37; 45pp; English.

XX

XX Growth of birds is increased by (a) admin. to the bird, in ovo,

CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.

CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

CC partic. Gly and the Thr normally adjacent to Glu can be replaced

CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced

CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the Thr normally adjacent

CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.

CC comprises the N-terminal given in R51450-53.

CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human

CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid

CC N-terminal extension.

XX Sequence 3 AA;

SQ

Query Match 75.0%; Score 9; DB 15; Length 3;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4

DB 3 C 3

RESULT 8

R51441

ID R51441 standard; peptide; 3 AA.

XX

AC R51441;

XX

DT 27-OCT-1994 (first entry)

XX

DE IGF-1 analogue N-terminal.

XX

KW Insulin-like growth factor; IGF-1; IGF-2; bird; chicken; egg;

KW in ovo; growth; promotion; increase; long R3 IGF-1; LR3 IGF-1.

XX

OS Homo sapiens.

XX

PN W09406445-A.

XX

PD 31-MAR-1994.

XX

PF 02-SEP-1993; 93WO-US08279.

XX

PR 17-SEP-1992; 92US-0947035.

XX

XX (EMBR-) EMBREX INC.

PA (GROP-) GROPEP PTY LTD.

PA (USDA) US SEC OF AGRIC.

XX

PI Ballard FJ, Francis GL, McMurtry JP, Phelps PV;

PI Walton PE;

XX

XX WPI; 1994-118144/14.

XX

XX Increasing growth of birds - with insulin-like growth factor

PT delivered to the egg before hatching esp. for increasing wt. gain

PT in chickens.

XX

PS Claim 6; Page 37; 45pp; English.

XX

XX Growth of birds is increased by (a) admin. to the bird, in ovo,

CC insulin-like growth factor (IGF)-1 or -2 or their active analogues;

CC (b) incubating to hatch and (c) growing the birds for at least 3

CC weeks after hatch.

CC IGF-1 analogues used pref. (i) lack 1-5 N-terminal amino acids or

CC (ii) have Glu(3) absent or replaced by Gly, Gln, Leu, Arg or Lys,

CC partic. Gly and the Thr normally adjacent to Glu can be replaced

CC by Arg or Gly. The IGF-1 analogue pref. comprises the N-terminal

CC given in R51439-49.

CC IGF-2 analogues used pref. have Glu(2) or Glu(3) absent or replaced
 CC by Gly, Gln, Leu, Arg or Lys, partic. Gly and the thr normally adjacent
 CC to Glu can be replaced by Arg or Gly. The IGF-2 analogue pref.
 CC comprises the N-terminal given in R51450-53.
 CC Esp. Long R3 IGF-1, given in R51454 is used. It is the full human
 CC IGF-1 sequence with Arg replacing Glu(3) and a 13 amino acid
 CC N-terminal extension.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 15; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
 |
 Db 3 C 3

RESULT 9
 W19847
 ID W19847 standard; Peptide; 3 AA.
 XX
 AC W19847;
 XX
 DT 23-SEP-1997 (first entry)
 XX
 DE Human interleukin-12 p40 subunit N-terminal peptide.
 XX
 KW Interleukin-12; Fc gamma-1; immunosuppressive; autoimmune disease;
 KW graft rejection; toxic shock; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9720062-A1.
 XX
 PD 05-JUN-1997.
 XX
 PF 02-DEC-1996; 96WO-US19181.
 XX
 PR 01-DEC-1995; 95US-0565856.
 XX
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 PA (UYMA-) UNIV MASSACHUSETTS.
 PI Steel AW, Strom TB;
 XX
 DR WPI; 1997-310615/28.
 DR N-PSDB; T72095-96.
 XX
 PT Fusion protein containing interleukin-12 p40 sub-unit - has
 PT increased stability, used to inhibit graft rejection, or treat
 PT autoimmune disease and endotoxin-induced shock
 XX
 PS Example; Fig 2; 36pp; English.
 XX

CC A peptide (W19847) comprises the three N-terminal amino acid
 CC residues of human interleukin-12 (IL-12) p40 subunit. It is
 CC encoded both by native human p40 cDNA (T72096) and by a primer
 CC (T72095) based on the native sequence. PCR amplification has
 CC been used to amplify p40 cDNA. A fusion protein comprising the
 CC p40 subunit and human Fc gamma-1 (see also W19853) was expressed
 CC in E. coli. This fusion protein has a longer in vivo half-life
 CC than native p40 and can be used as an immunosuppressive (e.g. to
 CC treat autoimmune diseases or to inhibit graft rejection) or to
 CC treat or prevent endotoxin-induced shock.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 18; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 C 4
 |
 Db 2 C 2

RESULT 10
 W56231
 ID W56231 standard; peptide; 3 AA.
 XX
 AC W56231;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Anti-inflammatory tripeptide.
 XX
 KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
 KW T-cell inhibitory activity; adherence; extracellular matrix;
 KW up-regulation; fas receptor expression; inflammation.
 XX
 OS Synthetic.
 XX
 PN WO9809985-A2.
 XX
 PD 12-MAR-1998.
 XX
 PF 03-SEP-1997; 97WO-IL00295.
 XX
 PR 28-MAY-1997; 97US-0864301.
 PR 03-SEP-1996; 96US-0025376.
 PR 20-NOV-1996; 96US-0753141.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
 XX WPI; 1998-193550/17.
 XX

XX Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease
 XX
 PS Claim 7; Page 35; 42pp; English.
 XX

CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
 CC Xaa = any amino acid residue.
 CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
 |
 Db 3 C 3

```

RESULT 11
ID W56211 standard; peptide; 3 AA.
XX AC W56211;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX DE Anti-inflammatory tripeptide.
XX KW Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN WO9809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX WPI; 1998-193550/17.
XX Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX Claim 6; Page 35; 42pp; English.
XX W56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be used
CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;
Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 C 4
DB 1 C 1
RESULT 12
ID W56200 standard; peptide; 3 AA.
XX AC W56200;
XX DT 20-JUL-1998 (first entry)

```

```

XX Anti-inflammatory tripeptide.
DE Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX OS Synthetic.
XX PN WO9809985-A2.
XX PD 12-MAR-1998.
XX PF 03-SEP-1997; 97WO-IL00295.
XX PR 28-MAY-1997; 97US-0864301.
XX PR 03-SEP-1996; 96US-0025376.
XX PR 20-NOV-1996; 96US-0753141.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
XX WPI; 1998-193550/17.
XX Anti-inflammatory peptides and derivatives - used for treating, e.g.
PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
PT shock, HIV infection, transplant rejection or Alzheimer's disease
XX Claim 5; Page 34; 42pp; English.
XX W56171-248 represent anti-inflammatory tripeptides of the invention.
CC They are derived from the formulae:
CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
CC Xaa = any amino acid residue.
CC Cyclic derivatives of the peptides also function as anti-inflammatory
CC agents. The peptides can be covalently linked to one another either
CC directly or through a spacer. The peptides and their derivatives have
CC macrophage inhibitory and T-cell inhibitory activity and thus,
CC anti-inflammatory activity. The peptides and compositions have
CC anti-immune activity, i.e. inhibitory effects against a cellular and
CC humoral immune response, including a response not associated with
CC inflammation. The peptides also inhibit the ability of macrophages and
CC T-cells to adhere to extracellular matrix components and fibronectin, as
CC well as up-regulated fas receptor expression in T-cells. They can be used
CC to inhibit unwanted immune reaction and inflammation.
XX SQ Sequence 3 AA;
Query Match 75.0%; Score 9; DB 19; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 C 4
DB 3 C 3
RESULT 13
ID W56172 standard; peptide; 3 AA.
XX AC W56172;
XX DT 20-JUL-1998 (first entry)
XX DE Anti-inflammatory tripeptide.
XX Anti-inflammatory; macrophage inhibitory activity; fibronectin;
KW T-cell inhibitory activity; adherence; extracellular matrix;
KW up-regulation; fas receptor expression; inflammation.
XX

```

OS Synthetic.
 PN WO9809985-A2.
 XX
 PD 12-MAR-1998.
 XX
 PF 03-SEP-1997; 97WO-IL00295.
 XX
 PR 28-MAY-1997; 97US-0864301.
 PR 03-SEP-1996; 96US-0025376.
 PR 20-NOV-1996; 96US-0753141.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Beserman P, Eisenbachschwartz M, Hirschberg DL;
 XX WPI; 1998-193550/17.
 DR
 XX
 XX Anti-inflammatory peptides and derivatives - used for treating, e.g.
 PT arthritis, ulcerative colitis, auto-immune disease, allergy asthma,
 PT shock, HIV infection, transplant rejection or Alzheimer's disease
 XX
 PS Claim 3; Page 34; 42pp; English.
 XX
 CC W56171-248 represent anti-inflammatory tripeptides of the invention.
 CC They are derived from the formulae:
 CC Xaa-Glu-Arg, Arg-Glu-Xaa, Xaa-Arg-Glu, or Glu-arg-Xaa, where
 CC Xaa = any amino acid residue.
 CC Cyclic derivatives of the peptides also function as anti-inflammatory
 CC agents. The peptides can be covalently linked to one another either
 CC directly or through a spacer. The peptides and their derivatives have
 CC macrophage inhibitory and T-cell inhibitory activity and thus,
 CC anti-inflammatory activity. The peptides and compositions have
 CC anti-immune activity, i.e. inhibitory effects against a cellular and
 CC humoral immune response, including a response not associated with
 CC inflammation. The peptides also inhibit the ability of macrophages and
 CC T-cells to adhere to extracellular matrix components and fibronectin, as
 CC well as up-regulated fas receptor expression in T-cells. They can be used
 CC to inhibit unwanted immune reaction and inflammation.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 19; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
 |
 Db 1 c 1

RESULT 14
 W88037
 ID W88037 standard; peptide; 3 AA.
 AC W88037;
 XX
 DT 09-APR-1999 (first entry)
 XX
 DE Peptide used in the hair composition of the invention.
 XX
 KW Hair; styling; wave.
 XX
 OS Synthetic.
 XX
 PN JP11012138-A.
 XX
 PD 19-JAN-1999.
 XX
 PF 18-JUN-1997; 97JP-0161657.
 XX

PR 18-JUN-1997; 97JP-0161657.
 XX (LIOY) LION CORP.
 PA
 XX WPI; 1999-148442/13.
 DR
 XX New composition for hair - comprises oligopeptide having more than 2
 PT cysteine residues and reducing agent
 PT
 XX Example 2; Page 6; 17pp; Japanese.
 PS
 XX Peptides W88033-39 are used in the hair composition of the invention.
 CC The specification describes a hair composition that comprises at
 CC least one oligopeptide having more than two cysteine residues and more
 CC than three amino acid residues of the same kind (except cysteine) and a
 CC reducing agent. The composition is useful for styling hair to take
 CC various shapes and waves safely and effectively.
 XX
 SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 20; Length 3;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
 |
 Db 1 c 1

RESULT 15
 Y51896
 ID Y51896 standard; peptide; 3 AA.
 XX
 AC Y51896;
 XX
 DT 16-JUN-2000 (first entry)
 XX
 DE Biostatin TT232 synthesising peptide 1.
 XX
 KW Solid phase synthesis; biostatin; cytostatic; tyrosine kinase inhibitor;
 KW cellular proliferation inhibition; somatostatin; antitumor.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "TFA*Lys(2)"
 FT Modified-site 2 /note= "Cys(Acm)"
 FT Modified-site 3 /note= "Thr(tBu) with C-terminal amide group"
 FT
 XX WO200011032-A2.
 PN
 XX 02-MAR-2000.
 PD
 XX
 PF 20-AUG-1999; 99WO-EP06131.
 XX
 PR 20-AUG-1998; 98WO-EP05306.
 XX
 PA (ORPE-) ORPEGEN PHARMA GES BIOTECHNOLOGISCHE FOR.
 XX
 PI Braum G, Lifferth A, Birr C;
 PI
 XX WPI; 2000-224663/19.
 DR
 XX Biostatin preparation in high yield by solid synthesis, including
 PT closure of disulfide bridge before cleavage from support, useful as
 PT antitumor agent
 XX
 PS Example 4; Page 23; 33pp; German.
 XX

CC This invention describes a novel method for the solid phase (SP)
CC synthesis of biostatin (TT 232) (I) which includes closing the disulfide
CC bridge by oxidation of the completely or partially constructed peptide
CC while still bonded to the solid phase. The products of the invention have
CC cytotstatic activity and are tyrosine kinase inhibitors. (I) inhibits the
CC tyrosine kinase activity of various human stomach cancer cell lines and
CC thus inhibits cellular proliferation. The heptapeptide (I) described in
CC the invention is a somatostatin analog which shows strong antitumor
CC activity in vitro and in vivo. The SP synthesis method gives (I) is more
CC easily and in markedly higher yield than by the method of EP505680, in
CC which the cyclization is carried out after cleaving the peptide from the
CC resin. The solution method is also a simple synthesis of (I) in high
CC yield; typically the tert-butyl-protected precursor can be oxidized in
CC a yield of 70-80%. Y51896-Y51900 represent peptides used in the
CC synthesis of biostatin TT232 described in the method of the invention.

XX

SQ Sequence 3 AA;

Query Match 75.0%; Score 9; DB 21; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
Db 2 c 2

Search completed: February 5, 2001, 12:01:19
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(without alignments)
2.324 Million cell updates/sec

Title: US-09-687-267-6
Perfect score: 12
Sequence: 1 XXXC 4

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /cgn2.6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/2/iaa/6_COMB.pep.*
- 4: /cgn2.6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 5: /cgn2.6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	75.0	2	1	US-07-791-213D-23
2	9	75.0	2	1	US-07-791-213D-39
3	9	75.0	2	1	US-08-133-804-9
4	9	75.0	2	1	US-08-354-240A-12
5	9	75.0	2	1	US-08-461-838-9
6	9	75.0	2	1	US-08-293-150A-23
7	9	75.0	2	1	US-08-293-150A-39
8	9	75.0	2	2	US-08-461-886-9
9	9	75.0	2	2	US-08-465-380-307
10	9	75.0	2	2	US-08-486-397-307
11	9	75.0	2	2	US-08-486-399-307
12	9	75.0	2	2	US-08-461-965-307
13	9	75.0	2	2	US-08-634-641-307
14	9	75.0	2	2	US-08-818-253-52
15	9	75.0	2	3	US-09-249-471-307
16	9	75.0	2	3	US-09-249-472-307
17	9	75.0	2	3	US-09-249-451-307
18	9	75.0	2	3	US-08-809-455-307
19	9	75.0	2	3	US-09-249-461-307
20	9	75.0	2	3	US-09-249-448-307
21	9	75.0	2	3	US-07-791-213D-22
22	9	75.0	3	1	US-07-791-213D-38
23	9	75.0	3	1	US-07-945-982-2
24	9	75.0	3	1	US-07-945-982-8
25	9	75.0	3	1	US-07-947-035-3
26	9	75.0	3	1	US-07-947-035-4
27	9	75.0	3	1	US-07-947-035-5
28	9	75.0	3	1	US-08-285-443-4

29 9 75.0 3 1 US-08-079-812-31 Sequence 31, Appl
30 9 75.0 3 1 US-08-122-510-11 Sequence 11, Appl
31 9 75.0 3 1 US-08-122-510-12 Sequence 12, Appl
32 9 75.0 3 1 US-08-122-510-13 Sequence 13, Appl
33 9 75.0 3 1 US-07-789-913-26 Sequence 26, Appl
34 9 75.0 3 1 US-08-371-930-4 Sequence 4, Appl
35 9 75.0 3 1 US-08-049-794-26 Sequence 26, Appl
36 9 75.0 3 1 US-08-372-455-2 Sequence 2, Appl
37 9 75.0 3 1 US-08-372-455-8 Sequence 8, Appl
38 9 75.0 3 1 US-08-321-585A-1 Sequence 1, Appl
39 9 75.0 3 1 US-08-321-585A-2 Sequence 2, Appl
40 9 75.0 3 1 US-08-321-585A-3 Sequence 3, Appl
41 9 75.0 3 1 US-08-446-908-14 Sequence 14, Appl
42 9 75.0 3 1 US-08-231-205A-14 Sequence 14, Appl
43 9 75.0 3 1 US-08-293-150A-22 Sequence 22, Appl
44 9 75.0 3 1 US-08-293-150A-38 Sequence 38, Appl
45 9 75.0 3 3 US-08-447-515-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-07-791-213D-23
; Sequence 23, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 C 4
       1
Db      2 C 2

RESULT  2
US-07-791-213D-39
; Sequence 39, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-39

Query Match      75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 C 4
       1
Db      1 C 1

RESULT  3
US-08-133-804-9
; Sequence 9, Application US/08133804
; Patent No. 5534254
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/133,804
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..2
; OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-133-804-9

Query Match      75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 C 4
       1
Db      2 C 2

RESULT  4
US-08-354-240A-12
; Sequence 12, Application US/08354240A
; Patent No. 5670356
; GENERAL INFORMATION:
; APPLICANT: Sherif, Bruce A.
; APPLICANT: Wood, Keith V.
; TITLE OF INVENTION: MODIFIED LUCIFERASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,240A
; FILING DATE: 12-DEC-1994
; CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506.029
TELEPHONE: 608-831-2100
TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-354-240A-12

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 1 C 1

RESULT 5
US-08-461-838-9
Sequence 9, Application US/08461838
Patent No. 5753204
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
IMAGING
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,838
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..2
OTHER INFORMATION: /note= "C-Terminal Tail (Ser-Cys)"
US-08-461-838-9

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 C 4
|
Db 2 C 2
RESULT 6
US-08-293-150A-23
Sequence 23, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-23

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 2 C 2

RESULT 7
US-08-293-150A-39
Sequence 39, Application US/08293150A

Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293.150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-39

Query Match 75.0%; Score 9; DB 1; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 1 C 1

RESULT 8
US-08-461-386-9
Sequence 9, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..2
OTHER INFORMATION: /note= "C-terminal Tail (Ser-Cys)"
US-08-461-386-9

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 2 C 2

RESULT 9
US-08-465-380-307
Sequence 307, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465.380
FILING DATE: June 5, 1995
CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/268
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.
US-08-465-380-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 1 C 1

RESULT 10
US-08-486-397-307
;; Sequence 307, Application US/08486397
;; Patent No. 5866542
;; GENERAL INFORMATION:
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
;; APPLICANT: Peter W. Bergum
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
;; TITLE OF INVENTION: PROTEIN
;; NUMBER OF SEQUENCES: 357
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,397
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/269
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.
US-08-486-397-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 1 C 1

RESULT 11
US-08-486-399-307
;; Sequence 307, Application US/08486399
;; Patent No. 5866543
;; GENERAL INFORMATION:
;; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
;; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
;; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
;; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
;; APPLICANT: Peter W. Bergum
;; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
;; TITLE OF INVENTION: PROTEIN
;; NUMBER OF SEQUENCES: 356
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; STREET: Suite 4700
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: U.S.A.
;; ZIP: 90071
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; MEDIUM TYPE: storage
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: IBM P.C. DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,399
;; FILING DATE: June 5, 1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/326,110
;; FILING DATE: October 18, 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIGGS, SUZANNE L.
;; REGISTRATION NUMBER: 30,158
;; REFERENCE/DOCKET NUMBER: 213/270
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 307:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; OTHER INFORMATION: Xaa in location 2 is an
;; amino acid.

US-08-486-399-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 1 C 1

RESULT 12

US-08-461-965-307
; Sequence 307, Application US/08461965
; Patent No. 5872098
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,965
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 210/243
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-461-965-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
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Db 1 C 1

RESULT 13

US-08-634-641-307
; Sequence 307, Application US/08634641
; Patent No. 5955294
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George P. Vlasuk
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Mensens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,641
; FILING DATE: April 19, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 219/136
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; amino acid.
US-08-634-641-307

Query Match 75.0%; Score 9; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 C 4
|
Db 1 C 1

RESULT 14

US-08-818-253-52
; Sequence 52, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-818-253-52

QY 4 C 4
|
Db 1 C 1

RESULT 15

US-09-249-471-307
; Sequence 307, Application US/09249471
; Patent No. 604041
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssems, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Beigum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,471
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FRAGMENT TYPE: internal fragment
; FEATURE:
; OTHER INFORMATION: Xaa in location 2 is an
; OTHER INFORMATION: amino acid.
US-09-249-471-307

Query Match

75.0%; Score 9; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 C 4
|
Db 1 C 1

Search completed: February 5, 2001, 12:01:54
Job time: 336 sec

